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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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1: pir1:*
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4: pir4:*
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1778
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                              opioid receptor mu opiate recep proteinase acti
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neuropeptide Y/per	S28787	ω ω	30	15.8	281.5	ū
interleukin 8 rec	JQ1231	(n	35	15.9	282	4
chemokine (C C) re	A43113	n	35	15.9	181	w
tusin (LESTRA)	000048	<del>د</del> ؛	35	15.9	282.5	i.
3 protein coupled	138974	3	ى نى	16.0	284.5	
neuropeptide Y/pep	A45747	to to	ني ئ	16.3	290.5	5
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G protein coupled	S33733	10	36	16.5	292.5	æ
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A. Molecule type. DNA A. Residues: 1-226, TG*,229-342SEY: A. (Fross-references: GR_MRR177; NID-glgg697: PIFN AAA*02]4.]; A)(Oross-references: GR_MRR177; NID-glgg697: PIFN AAA*02]4.]; A)(Note: Sequence extracted from NCBI backbone (NCBIN:109813; R)(Chase, P.B.; Halonen, M.; Regan, J.W. Am. J. Respir. Ceil M.J. Biol. 8, 240-244, 1993	A, Residues. 1.315, YM., 317-342 <sug> A, Residues. 1.315, YM., 317-342 <sug> A, Experimental source: heart A, Note: the authors translated the codon AAT for residue 316 as Lys R, Seytried. C.E., Schweickart, V.L., Godiska, R., Gray, P.W. Genomics 13, 832-834, 1992 A, Title: The human platelet-activating factor receptor gene (PTAFR) contains no A, Reference number. A42831; MULD.92347886 A, Accession: A42831</sug></sug>	A, Status: not Compared with conceptual translation A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1 342 kNAKS A, Closs reterences. GB.Dloud.; GB.D90433; NID:q219975; PIDN:BAA01050.1; PID:q219976 R, Sugimeto, T.; Tsuchimechi, H.; MoGregor, C.G.A.; Mutoh, H.; Shimizu, I.; Kurachi, Y. Hiochem Biophys Res. Commun. 189, 617-624, 1992 A, Title, Molecular clouding and characterization of the platelet activating factor tech. Research of the number: JC1359; MUID:93112021 A, Research of the platelet activation of the platelet activating factor tech. Receasion, JC1359; MUID:93112021	A; Molecule type: mRNA A, Residues i 342 yttm. A, Residues i 542 yttm. A, Residues i 542 yttm. A, Cross references: GR: M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538 A, Experimental source: granulogyte, cell line H: 60 all R, Nakamura, M, Honda, Z.; Izumi, T.; Sakanaka, C.; Mutch, H.; Minami, M.; Bito. R, Nakamura, M, Honda, Z.; Izumi, T.; Sakanaka, C.; Mutch, H.; Minami, M.; Bito. A, Title: Molecular cloning and expression of platelet-activating factor receptor A, Reference number: A41079; MUID:g2041873 A, Accession: A41079	RESULT 1 A40191 A40191 PlateLet-activating factor receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo Apole; Sequence_revision 28 Aug 1992 #text_change 20 Jun 2000 C;Accession A40191; JH0479; A41079; J71389; A42831; I51923 R;Kunz, D.; Gerard, N.P.; Gerard, C. J. Biol. Chem 267, 9101-9106, 1992 A;Title: The human leukocyte platelet activating factor receptor. cDNA cloning, cell A;Reference number: A40191; MUID:92250505 A;Residues: A40191 A;Molecule type: mRNA A;Residues: 1-342 <kun> A;Cross-references: GR-M76674; NID:9456293; FIDN-AAA60002 1; PID:9446294 R;Ye, R.D; Prossnitz, F.R.; Zou, A.; Cochrane, C.G. Riochem Hiophys Res Commun 1Hn, 105-111, 1991 A;Beterence number: JH0479; MUID:92028922 A;Accession: JH0479; MUID:92028922</kun>	ALI CNMENTS	35 296.5 16.7 200 2 151567 36 296.16.6 380 2 536143 37 295 16.6 380 2 536143 37 295.5 16.6 360 2 533738 38 292.5 16.4 373 2 A47556 40 290.5 16.3 352 2 A45747 41 284.5 16.0 333 2 138974 42 282.15.9 352 2 138974 43 282 15.9 352 2 A43113 44 282 15.9 352 2 A43113 45 281.5 15.8 353 2 528787
-AAA+0214.1; PID:q190698 CBIN:109813; NCBIP:109814)	residue 316 as Lys , Gray, P.W. ceptor gene (PTAFR) contains no intro	on 19975; PIDN:BAA01050.1; PID:q219976 .: Mutch, H.: Shimizu, H.: Kurachi. Y of the platelet activating factor rec	:AAA60001.1; PID:g189538 -60 all C.; Mutob, H.; Minami, M.; Bito. H.; Lelet-activating factor receptor from	92 #text_charge 20 Jun 2000 factor receptor, chWA cloning, cell factor receptor, chWA cloning, cell factor receptor, chWA cloning, cell factor receptor for plat		throubin receptor throubin receptor kappa opioid receptor kappa opioid receptor kappa opioid receptor kappa opioid receptor for the first Plus in (LISTRA) capentarin (LISTRA) capenokine (C.C.) reinterleakin 8 recepted interleakin 8 recepted interleakin (C.C.)

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A:Cross reterences, GDB,128806,
A:Map position: 1p45 1p34,3
A:Map position: 1p45 1p34,3
C:Supertamily: ATP receptor Pau
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A.Reference number: 191928; MUID:93192039
A.Accession: 191928
A.Status: proliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1 42 - RES
                                                                                                                                                                                                                  A:Cross-reterences: GB:X56736: NID:q49442; PIDN:CAA40060.1; PID:q49443 A:Note: the species of quinea pig is not identified; in GenBank entry CCPAFREC, release C:Supertamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Cloning by functional expression of platelet-activating factor receptor from gr
A:Reference number: $13638; MUID:91101726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Honda, Z.: Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, Naturo 349, 342-346, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: Slabas
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C:Date: 19 Mar 1997 #sequence_revision 19 Mar-1997 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                 A) Residues: 1 342 - HoN.
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                                                                                       Query Match
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5/4 75/Domain: transmembrane #status predicted <TII-
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                     Matches 103;
                                                    Best Local Similarity
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297/Numarin: transmembrane #status predicted <VII-
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                 Conservative
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                                                22.1%; Score 392.5; DH 2; Length 342; 30.7%; Pred. No. 2.18-26;
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                 Mismatches
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             146;
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             Indels
             <u>:</u> :
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    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: nucleic acid
A;Residues: 1-361 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A45680; MUID:93188173
A;Accession: B45680
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C; Accession: B45680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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    262 STLWLTSLNACLDFFLYFFLCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETF 341
                                                                                                                               236 SGVNK---KALNT-HILHIVVFVLCFTPYHVAHOHMIKKERFSNFLECSQRHSFGISLH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 SISFLALITIDRYOKTTPPFKTSNPKNLLGAKTI SVVIWAFMELLSLPNMI - -LINROPR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 INSTITLYSTALVISDILFTTALPTRIAYYAMGFDWKIGDA-----LCRITALVFYINTYA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MQAVDNLT----SAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFOIRSK 56
                                                                                                                                                                                                              RGVGKVPRKKVNVKVFIIIAVFFICFVPFHFAPIPYTISQTP--DVFDCTAENTLFYVKE 281
                                                                                                                                                                                                                                                                                             RITCMEYPNFEETKSLPW--ILLGACFIGYVLPLIIILICYSQICCKLFRTAKQNPLTEK 23°
                                                                                                                                                                                                                                                                                                                                                                            DKNVKKCSFLKSEFGLVMHETVNYTCQVTFWTNFLTVTVCYTETTKELYRS-----YVRT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVNEMTCLSIDREIAVVHPLRYNKIKRIEHAKGVCIEVWILVFAQTLPLLINPMSKQEAE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SN-FIIFLKNTVISDLLMILTFPFKIL-----SDAKLGTGPLRTFVCQVTSVIFYFTMYI 110
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J. Virol. 67, 2209-2220, 1993
A/Title. Epstein Barr virus induced genes. first lymphocyte-specific G protein comple
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C;Date: 21 Sep 1993 #sequence_revision 18 Nov 1994 #text_change 21 Sul 2000
A:Cross:references: GB:108177, NID:g292056, PIDN:AAA35924.1, PID:g292057
                                                                                                                                                                                                                                                                                                                                                        R;Hirkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 ICEVPHHMVQLEWTLAEL-GMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 ICEVPEHFARIPYILSQTROVEDCTAENTLEYVKESTLWLTSLNACLDPFIYFFLCKSER
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R:Bito, H.: Honda, Z.: Nakamura, M.: Shimizu, T.
Eur. J. Biochem 221 -218, 1994
A:Rifitle: Clenie, expression and tissue distribution of rat platelet activating factor
A:Reference number: $43252; MUTD:94222063
                                                                                                                                                                                                                                                                                                                                                                                                                   platelet-activating factor receptor—rat
C:Species: Rattus norvegicus (Norway rat)
C:Date 20 Fet 1974 #sequence revision in Nov 1975 #text_change 24 Nov
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C:Species: Mus musculus (house mouse)
C:Date: 28-oct-1996 #sequence_revision 14 Mar-1997 #fext_change 28-him-2800)
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                                                                                                                          A:Cross-reterences: GR-H04740: NID-9470384; PIDN-AAA18422
C:Superfamily: ATP receptor P2u
                                                                                                                                                                                   A: Molecule type: mRNA
A: Residues: 1-341 <BI
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;Cross_references: EMBL:050872; NID.gl256924; FIDN.BAA09468.1; FID.gl256925
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      Best Local Similarity
                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 M 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 CFVPHHVVQLFWILAELG--YQ1NFHQAINDAHQITLCLLSTNCVLDPVIYCFLTKKFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 CFYPFHFARIPYTLSQTBDYFDCTAENTLFYVKESTLWLTSLNACLDPF1YFFLCKSFEN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 TRKRG1SLSL11WVS1VATASYFLATDSTNLVPNKDGSGN1TKCFEH1EPYSVF1LVVHV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 NLLGAKILSVVIWAFM
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Local Similarity 29.9%; Pred. No. 4.1e-24;
hes 96, Conservative 64; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 M 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 HISEKFYSMRSSRKC-SRATS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 -----SLISMLKCPNSATS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 IVNYICOVIEWINELI-VIVCYTLITKELYRSYVETROVGKVPEKKVNVKVEIIIAVEEI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 LPLWIVYYYNEGDWILPNFLCNVAGCLFFINTYCSVAFLGVITYNRYQAVAYPIKTAQAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 FPFKILSDAKLGTGPLKTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 DSEFRYTLFPIVYSVIFILGVVANGYVLWVFANLYPSKKLNEIKIEMVNLIMADLLFLIT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 DYKITQVLEFLLYIVLEEVGLITNGLAMKIEEGI--RSKSNET-IELKNTVISDLIMILT 76
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                                                                                                                                                                                   1-341 <BIT>
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      20.4%;
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   Pred. No.
                                  Score
                                  362;
         90-24:
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                               DB 2;
                                  Length 341.
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                                                                                                                                                                                                                                                                                                                                                                                                                G:Superfamily: ATP receptor P2u C:Keywords: G protein coupled receptor; transmembrane protein E:15-40/Jonnain: transmembrane #status predicted <TM1> F:51-74/Jonnain: transmembrane #status predicted <TM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 믕
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                                                                                                                                                                                                                                                                     F:133-153/Domain: transmembrane #status predicted <TM4>
F:137-201/Domain: transmembrane #status predicted <TM5>
F:227-248/Jounain: transmembrane #status predicted <TM5>
F:269-292/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A, Title: Identification of 6H1 as a P2Y purinoceptor. P2Y5
A;Reference number: JC4618; MULD:96190677
A;Accession: JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Relerence number: I50241; MUID:93329058
A; Accession: I50241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02 Jun 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GB:L06109; NID:g304383; PIDN:AAH05587.1; PID:g304384
A,Experimental source: T-cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: 150241; JC4618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: p2Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Comment. This receptor plays a role in T-cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-308 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Residues: 1-308 -KAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mkNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A: Title: Identification of a d protein coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Crossireferences: 3B:L06109; NTD:3364383; PIDN:AAR06587.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K, Kaplan, M.H.; Smith,
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 IYCELTKKERKHLSEKFYSMRSSRKC-SRATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 IYFFLCKSFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 KVFIITAVFFICFVPFHFAPIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLINDF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 FITSCFFLVFF-----LIFYCNMVII---HTLLTRP-----VKQQRKPEVKRRALMM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 FLKSEFGLVWHELIVNYTGOVIFWINFLIVIVCYTLITKELYKSYVKTRGVGKVFKKKVNV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 - VCTVLAVEVICEVPHHVVQL#WTLABLG--YQINFHQAINDAHQITLCLLSTNCVLDPV-290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                           14 TSLCTRDYKITQVLEPILYTVLEFVGLITNGLAMRIF-FQIRSKSNEIIFLKNTVISDIL 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 DSEFRYTLEPIVYSVIEVLGVVANGYVLWVFATLYPSKKLNEIKIEMVNLTVADLLELMT 69
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3 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL 62
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                                                                                                                    al Similarity
87; Conserv
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.I.; Sundick, R.S.
                                                                                                                                                    20.1%;
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                                                                                                                          68; Mismatches
                                                                                                                                             Score 357.5;
Fred. No. 2e
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                                                                                                                                                                             DB 2; Length 308;
                                                                                                                    125; Indels
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                                                                           C; Species: Homo sapiens (man)
                                                                                                   intron 17 purinerqie receptor P2Y5 human
N:Alternate names: G protein coupled receptor
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A:Cross references: GB:X5/2294; NID:q43; PIDN:CAA44182.1; PID:g44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Accession: S15403
R:Sasaki, K.: Yamano
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                                                                                                                                                                                                                                                                313 FLOLLKYTPPKAKSBONI STKMSTI SYPPOPNONSSTKKP (32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 VIEWINELIVIVCYTLITKELYRSYVRTROVOKVPRKKVNVKVEIIIAVEEICEVPEHEA 255
                                                                                                                                                                                                                                                                                                              109 LISMIK CPNSAISLSODNEK-
                                                                                                                                                                                                                                                                                                                                                                    254 WVFHQTFTEMDVLTQLGLIKDCKTEDTVDTAMFTTTCLAYFUNGLUPLFYGFLGKKFKKY 312
                                                                                                                                                                                                                                                                                                                                                                                                                     256 RIPYTLSQTRDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 CHTMITAGLASUPTITHENVEFTENTNITVCAFHYESQNSTEPVGLGET-KNILGFL-- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 SVVIWAEMELLSLENMILIEN KOPRDKNVKKOSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 EVPYNITLILYSLMHTQTWINGSVVTAVPTMYPV - TLCIAVSNCCEDPIVYYF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 FVPEHEARIPYTLSOTROVEDO -TAENTLEYVKESTLWITTSLNACIDPETYEE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 IVIETETVGEETPLILNVTGSTMVLRFLNKPDFLSK--NKLSKKKVLKMIFVHLVTFCEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 IVNYIOGVIEWINELIVIVOYTLITKELYESYVETEGVGKVEEKKVNVKVEIIIAVEEIC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 KILETKRNARIVOVAVWITVIAOSTPASEFOSTNRO-NNTEQRICEENFESTWETYLSR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 SNPKNLLGAKTLSVVTWAFMFILISLPNMTH "TNKQPRDKNVKKC" - SFLKSEFGLVWHE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 EVETLEFRIYYEV-VRNWPFGDVLCKISVTLEYTNMYGSILFLTGISVDRFLAIVHPERS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY AMEYRWEEGNYLOKIASASVSENLYASVELLTOLSIDRYLAIVHPMKSRLRRTMLVAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 AKLGTGPLRTEVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 IMEPTLYSTEFVVGTEGNSLVVTVTYFYMKLKTVASVELLNLALADLCELLTLPLWAVYT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 VLEPLLYTVLEEVGLITNGL-AMRIFFQIRSKSNFIIELKNTVISDLLMILTEPFKILSD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 MILTEPEKILSDAKLGIGPLETEVCQVTSVIFYFIMYISISFLGLITIDRYQKTTRPEKT 132
S.K.: Frumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95; Conservative 62, Mismatches 143; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - FEED COLUMN TORKAYELOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.1%; Score 339; DH 2; 27.9%; Pred. No. 9.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                  · DOTAFNTLFYVKESTLWLTSLNAGLDFFTYFFLGKSFRNS 308
                                                                                                                                                                                                                                                                                                              - KEODGGDPNEETP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ***NKPKKDDIFKITIAIVIFFF**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kuroda, S.
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                                                                                                                                                                                                                                                                                   Query Match
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                                                                           85
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A:Map position: 13
C:Superiamily: ATP receptor P2u
C:Keywords: G protein coupled receptor: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Phsidues: 1-359 (RES)
A;Cross-references: GR:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 199, 467-474, 1994
A;Title: Novel subtype of human anglotensin II type I receptor: cDNA cloning and expr
A;Reference number: I39418; MOID:94183213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiotensin II receptor type 1b - human
C;Species: Homo sapiens (man)
C;Datc: 29-May-1998 *scquence_revision 29 May 1998 *text_change 24-Nev 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-344 < BOH>
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A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the reti
A;Reference number: Z16705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary, translated from GB/EMBI/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 QNS----IKMKNWSVRRS-DFRFSEVHGAE 323
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89 AMEYRWIPFGNYLCKTASASVSFNLYASVFILITCLSTDRYLATVHPMKSRLRKTMLVAKVI 148
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                                                                                                                                                                      29 VMIPTLYSTIFVVGTFONSLVVTVTYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT 88
                                                                                                                                                                                                                                                   26 VI.FPILLYTVI.FFVGI.ITNGI. AMRIFFQIRSKSNFIIFI.KNTVISDI.MILITEFKIIISD 84
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                 AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
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                                                                                                                                                                                                                                                                                                                                                                                      18.5%; Score 329; DB 2; Length 359; 28.7%; Fred. No. 6.76 21;
                                                                                                                                                                                                                                                                                                                                                  58; Mismatches 137; Indels
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C:Species: Mus musculus (house mouse)
C:Date: 02 Jul 1996 #sequence_revision 02 Jul-1996 #text_change 24-Nov-1999
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S44425
        R:Nystedt, S.: Larsson, A.K.: Aberg, H.: Sundelin, J. Biol. Chem. 270, 5950-5955, 1995
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C:Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 343, 146-150, 1994
A;Title. Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A;Reference number: S44425, MUID.94222188
A;Accession: S44425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
Date: 19-Mar-1997 #sequence_revision 19 Mar-1997 #text_change 24-Nov-1999
Accession. S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
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                                                              C; Accession: 148705
                                                                                                                                             proteinase activated receptor 2 - mouse
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A:Residues: 1-359 <BUR>
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                                                                                                                                                                         148705
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                                                                                                                                                                                                                                                                                                                                 315 -CPNSATSLSQDNRK 328
                                                                                                                                                                                                                                                                                                                                                                                    259 FTFLDVLIQLGITHDCKTADTVDTAMPTTTCTAYFNNCLNPLFYGFLGKKFKKYFLQLLK 318
                                                                                                                                                                                                                                                                                                                                                                                                                                       255 ARTPYTLSQTRDVFDCTAENTLFYVKESTLMLTSLNACLDPFTYFFLCKSFRNSLISMLK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FPFLIILTSYTLIWKTLKRAYEIQK---NKPRNDDIFKIIMAIVLFFFFSWVPHQI 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.3%; Score 326, DB 2, 29.2%; Fred. No. 1.2e-20;
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145 SVVIWAFMFLLSLPNMILIN-RØFRDKNVKKCSF-----LKSEFGLVWHEIVNYICO 195
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R:Burns, K.D.: Inagami, T.: Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex ATI angiotensin II receptor that is presen
A:Reference number: A48857; MUID:93236091
A:Accession: A48857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiotensin II receptor type 1 - rabbit
C.Species: @ryctulagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18 Nov 1994 #fext_change 08-0ct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Title The mouse proteinase activated receptor 2 sDNA and gene. Molecular cloning a A:Reference number: 148795; MUID:95197820
A:Accession: 148705
                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: vertebrate rhodopsin
C;Keywords. G protein coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cress-references: GR-S59041; NID 9299614; FIRN-AAR26239 1; FID:9299615
A;Experimental source: proximal tubule cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIP:129601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues, 1:359 <80R>
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A; Residues: 1-399 < RES>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 KCPNSAT-----SLSQDNRKKEQDGGDPNEET 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 LLVVHYFLIKTO-----RQSHVYALYLVALCLSTLNSCIDFEVYYFVSKDFRDHARNAL
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                                                                                                                                                                                                                                          81 ILSDAKLGTGPLRTEVCQVTSVIEYETMYISISELGLITIDRYQKTTRPEKTSNPKNILG 140
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                                                                     29
                                                                                                                                    26 VLEPLLYTVLEEVGLITNGLA-MRIEFQIRSKSNFITELKNTVISDILMILTEPEKTISD 84
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AKEGEGPEKTEVCQVTSV1EYFTMYTS1SFEGELTIDRYQKTTKFFKTSNFKNELGAKIL 144
                                                                     VMIPTLYSIIFVVGIFGNSLAVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR-IPYTLSQTKDVFDCTAENTLFYVKESTLWLISLNACLDFFIYFFLCKSFRNSLISML 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGVELEPALLTASAYVLMIKTLRSSAMDEHSEKK--RQRAIRLIITVLAMYFICFAPSNI. 307
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AMEYRWPEGNYLCKIASASVSENLYASVELLICLSIDKYLAIVHPMKSKLKKTMLVAKVT 148

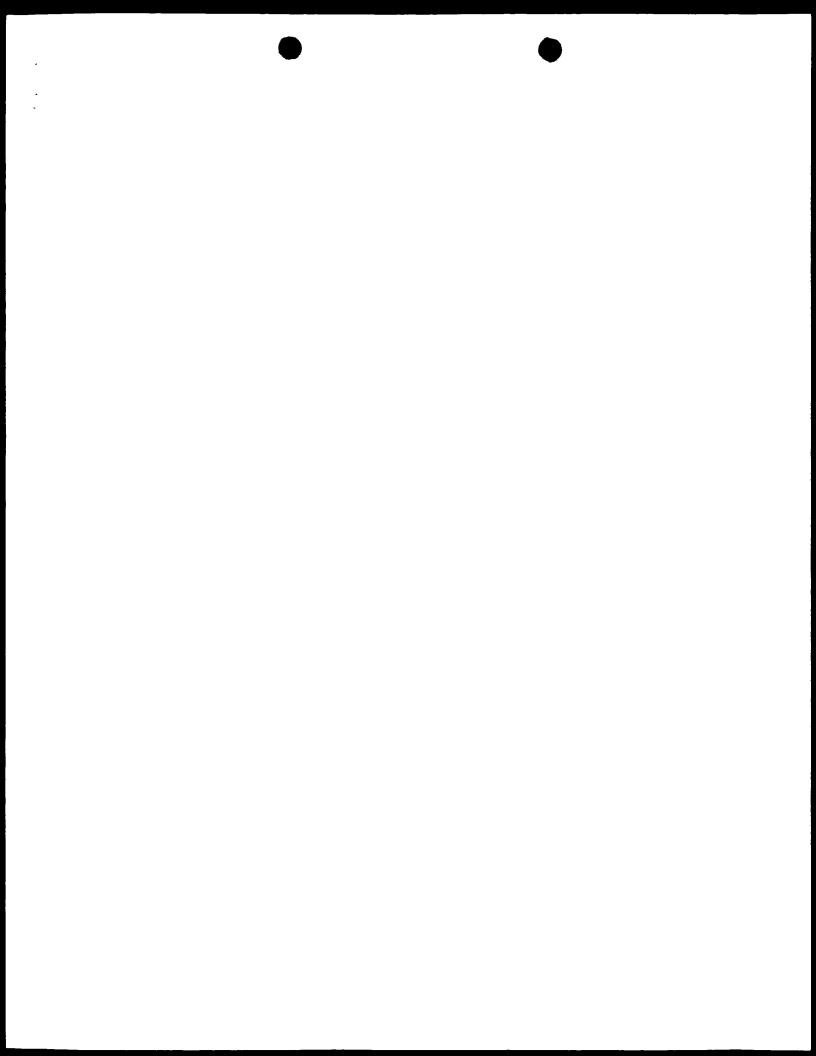
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A:Reference number: JC1104; MD1D:92397608
A:Revession: JC1104
A:Reference number: JNA
A:Residures: [ 359 - MAG) -
REFurnta, H.: Sub, D.F.; Endpami, T.
REFurnta, H.: Sub, D.F.; Endpami, T.
REFurnta, H.: Sub, D.F.; Endpami, T.
A:Revinta, H.: Sub, D.F.; Endpami, T.
A:Revision: JU1402
A:Revision: JU14
C:Supertamily: vertebrate rhodopsin
C:Keywords: C protein coupled receptor; dlycoprofern; hormone receptor; transmembrane pr
F:30 53/Domain: transmembrane #status predicted <TMT>
                                                                                                                                                                                                                                                                                                            A:Molecule type: mRNA
A:Mestidues: 1 359 -CMR.
A:Mostidues: 1 359 -CMR.
A:Mole: references: GMR.M93394: NID:q178680; PID:q178681
A:Nole: Sequence extracted from NCHI backbone (NCHIN:111831, NCHIP:111833)
C:Genetics:
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A:Reterence number: JH0267: MUID:92198490
A:Accession: JH0267
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A:Fille: Cloning and characterization of a human angiotensin II type I receptor. A:Reference number: JH0574, MHID:92241907
A:Accession: JH0574
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                                                                                                                                                                  A: Tross references: GDB:132359; OMIM:106165
A:Map position: 3q21 3q25
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A;Status: proliminary
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A:Title: Genetic analysis of the human type-1 angiotensin II receptor
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A:Residues: 1 859 - BER -
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A; Molecule type: DNA
A; Residnes: 1-370 <JAN>
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Best Local :
                   185 -- VWHETVNY I CQVI FWI NELLI VIV---- CYTLITKELYR---- SYVRI RGVGKVPRKKV 234
                                                                                                                                                             140 IVYPEPSPTIPTPPNSA1VCAGVWILVLSGGISASLEST-----TNVNNATTTGEE-GLS-194
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                                                                                                                                                                                                                                                           126 TERREKESNEKNLLGAKTLSVVTWAEMELLSLENMITTNROPEDENVKKUSETEKSEEGT - 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 LISMLK-CPNSATSLSQDNRK 328
                                                                                                                                                                                                                                                                                                                                               81 LAVSDLLFVCTLPFKIFYNEN-RHWPFGDTLCKISGTAFLITNIYGSMLFLTCISVDRFLA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                       66 TVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVISVIFYFTMYISISFIGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LGNATANNIT-CIVUUSEKYNLNGAVYSVVEILGLIINSVSLEVECERMKMKSEIAIFIIN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%; Score 321; DB 2; Length 370;
27.7%; Pred. No. 3.4e 20;
ative 67; Mismatches 134; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
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E:103-124/Domain: transmembrane #status predicted <TM3>
E:145-167/Domain: transmembrane #status predicted <TM4>
E:144-215/Domain: transmembrane #status predicted <TM5>
E:241-264/Domain: transmembrane #status predicted <TM6>
E:281-305/Domain: transmembrane #status predicted <TM6>
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253 WIPHQIFTFIDVLIQIGIIRDCRIADIVDTAMPITICIAYENNCINFLFYGFIJKKFKRY 312
                                                                                           256 KTPYTLSQTRDVF-------OCTAENTLEYVKESTLWIJTSLNACLDPFTYFFLCKSFRNS 308
                                                                                                                                                                                       206 ----FPFLIILTSYTLIWKALKKAYEIQK---NKPRNDDIFKIIMAIVLFFF-----FS
                                                                                                                                                                                                                                                                                        196 VIEWINELIVIVOVILLIKELLYKSYVKIKGVGKVEKKKVNVKVEIIIAVEEICEVEEHEA 255
                                                                                                                                                                                                                                                                                                                                                                                         149 CITIWILLAGIASLPATTHRNVFFTENTNITVCAFHYESQNSTLPTGI.GITT-KNILIGFI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 AMEYRWPFGNYLCKIASASVSFNLYASVELLTCLSIDRYLAIVHPMKSKLRRTMLVAKVT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%; Score 321; DB 2; 28.7%; Pred. No. 3.3e-20;
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RiJanssens, R.: Boeynaems, J.M.: Godart, M.: Communi, D.
Biochem Biophys Res Commun 236, 106-112, 1997
A.Title Cloning of a human heptabelical receptor closely related to the EEYS receptor
A:Cross-references+ DDB*-AF005419; NID:g2249034; FIEN:\Delta AR66322.11; FID:g2240035 C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species. Homo sapiens (man)
C:Date: 02 Sep:1997 #sequence_revision 05:Sep:1997 #text_change 24-Sep:1999
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Job time: 158 sec

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A:Molecule type: mRNA
A:Pesidues: 1:459 < LMA >
A:Cross-reletences: GB:X64052: NID:q57521: PIDN:CAA45410.1; PID:q57522
A:Cross-reletences: GB:X64052: NID:q57521: PIDN:CAA45410.1; PID:q57522
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Note: sequence extracted from NCB1 backbone (NCB1N:100262, NCB1P:100268)
R;Iwai, N.; Inaqami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423; MUID:92183879
A:Accession: $20423.
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NyAlternate names: angiotensin 11 receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #Sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A42656; S20423
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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAN>
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A:Experimental source: adrenal cortex
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A.Titlo. Cloubing and expression of a novel anglotensin II receptor subtype. Reference number: A42656; MUID:92250585
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A42656
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                                                                                                                                                                                                                                                                                                                                                                                             149 CITIWILMAGLASI.PAVIYRNVYFIENTNITVCAFHYESQNSTLPIGLGLT-KNILGFV--
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                                                              312 MLK-CPNSATS 321
                                                                                                                            256 HOLFTFLDVLLQLGLIRDCELADIVDTAMPITICIAVENNCLNPLFYGFLGKKEKKYFLO 315
                                                                                                                                                                                       252 FHEARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLIS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 SVVIWAFMFILSIPNMILTNRQ-PROKNVKKOSF-----LKSEFGLVWHEIVNYICQ 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
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LLKYIPPTAKS 326
                                                                                                                                                                                                                                                         ----FPFLIILTSYTLIWKALKKAYKIQK---NTPR---NDDIFRIIMAIVLFFFFSWVP 255
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090026 L Q924T8 Q9PUA0 Q9H573 09MYW9

Q9pua0 acipenser r Q9h574 homo sapien Q9myw9 macaca mula Q9eqr9 meriones un

⊖35811 rattus norv ⊖9udz6 homo sapien

0924t8 rattus norv

11 61 6 4 6

Ognoul ovis aries
Ogne21 homo sapien
Ogno2 sus scrota
Ogep3 cavia porce
Ogep4 pan trodlod
Ogj37 mus musculu
Ogj64 macuca tase

0920A1 09PVY7 09024T9 0900U1 090E21 095N02 095N02 095P03 09G,N9 109JUS7 10

309 309 308 307 304.5 304.5 304.5 304.5

09FQR9 09JJ71 099JA4 09R1M0 09R1L9 09R0D1

09r1m0 mus musculu 09r119 mus musculu 09r0d1 mus musculu 09jj71 mus musculu 099ja4 mus musculu

ALIGNMENTS

356 347.5 347.5

29XSD4 3 057466 29HCQ2 09NS75

Q9hcq2 homo sapien Q9ns75 homo sapien 09x5d4 Sub scruta 057466 meleagris g 09tty6 canis tamil 095m04 sus scruta

09pvy7 anguilla an 0924t9 rattus norv Q920al mus musculu 20N260

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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SP_Archea:*
Sp_barchea:*
Sp_barchea:*
Sp_barchea:*
Sp_lund:*
Sp_human:*
Sp_mamma'
T. Sp_mamma'
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1555.5
1528.5
829
741.5
694.5
694.5
553.5
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388.5
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1748
Match Length DB
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Listing first 45 summaries
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1 MQAVDNLTSAPGNTSLOTED
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sp_virus:*
sp_vertebrate:*
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                                                                            Q95kc3 macaca fasc
Q9cpv9 mus muscullu
Q9cpv4 raftus norv
Q9bpv8 homo sapien
Q9d812 mus musculu
Q9esg6 mus musculu
C96j28 homo sapien
Q9by21 homo sapien
Q9by21 homo sapien
Q9gmt7 mus musculu
C9bp53 macaca fasc
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"Molecular cloning of the platelet P2TAC ADP receptor;; Pharmacological comparison with another ADP receptor, the P2Y1	Soga T., Matsushime H., Furuichi K.;	Takasaki T. Kamohara M., Saito T., Matsumoto M., Matsumoto S.,	MEDLINE: 21/84281; FubMed-11502873;	SEQUENCE FROM N.A.	[3]	J Biol Obom. 276-8608-8615(2001).		"ADP is the cognate ligand for the orphan G protein-coupled receptor		G., Pramanik B., Laz T.M., Palmer K., Bayne M.,	Zhang F.L., Luo L., Gustafson e., Lachowicz J., Smith M., Qiao X.,	MEDLINE=21269433; PubMcd=11104774;	SEQUENCE FROM N.A.	[2]	Nature 409:202-207(2001).		"Identification of the Platelet ADP Receptor Targeted by	Conley P.B.;	rden A.	Hollopeter G., Jantzen HM., Vincent D., Li G., England L.,	MEDLINE-21037966; PubMed-11196645;	SEQUENCE FROM N.A.			Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	HORK3.		LET ADP RECEPTOR	(TrEMBLrel. 19,	(TrEMBLrel. 16,	01-MAR-2001 (TrEMBLrel. 16, Created)	~	Q9H244 PRELIMINARY; FRT; 342 AA.	4.4	LT 1

44400

Cobes a

Q9BXC2

Q9BY61 Q9TTY5 Q9GK76

Others homo sapien Q9by61 homo sapien Q9tty5 bos taurus

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Best Local :
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                                                                                                                                                                                            osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hiral M., Suzuki Y., Suqano S., Hashimoto K.;
"Isolation of full length cDNA clones from macaque brain cDNA libraties.";
                                                                                                                    Submitted (FEB 2001) to the EMBL/Genbank/DDBJ databases EMBL: AB055385; BAB33041.1; ; Interpro; IPR000276; GPCK_Rhodpsn. PF00001; 7tm.1; 1.
                                                                                                                                                                                                                                                                                                                                                     Macaca tascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Cercopithecidae;
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Ol-JHN 2001 (TrEMBLIP). 17, (realed)
Ol-JHN 2001 (TrEMBLIP). 19, Last sequence update)
Ol-JHP 2001 (TrEMBLIP). 19, Last annotation update)
HYPOTHEFICAL 49.5 KDA PROTEIN.
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                                                                    Hypothetical protein
                                                                                                     PRINTS: PRO0237: GPCKRHODOPSN
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Pfam: PPr00001; 7tm 1; 1.
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                                                     SEQUENCE
                                                                                    PROSTIE: PS50262; d_PROTEIN_RECEP_F1_2; 1.
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Q95KC3;
Q95KC3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 39.5 KDA PROTEIN.
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Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab eating macaque) (Cynomolqus monkey).
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleoste
Mammalia; Eutheria; Primates; Catarrhini; Gercopithecidae;
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NCBI_TaxID-9541;
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                                                                                                                                           DRYQKTTRPFKTSNPKNLLGAKILSVLIWAFMFLLSLPNMILTNRRPRDKNVKKCSFLKS
                                                                                                                                                                                                                                                                                       IELKNTVISDLLMILTEPEKILSDAKLGAGPLRTEVCQVTSVIEYETMYISISELGLITI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFLKNTVISDLLMILTEPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI
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98.0%;
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 Mismatches

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Pred. No. 1.6e-148
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3: Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6e-148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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01-JUN 2001 (TrEMBLrel 17, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
492150402381K PROTEIN (290007982281K PROTEIN)
P2RYL2 OR 4921504F23FIE OR 290007982281K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STEALN-057HL/6J; TISSUE-TESTIS, AND HIPPOCAMPUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia: Eutheria: Rodentia; Sciuroqnathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CPV9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21085660; PubMed-11217851;
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MGD; MGI:1920308. 2920279B22Fik
InterPro; TPR000276; GPCR_Rhodpsn
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EMBL: AK014807; BAB29561.1; -.
EMBL: AK013804; BAB29000.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 HAVEFICEVPEHEARIPYTLSQTRDVEDCTAENTLEVVKESTLMLTSLNACLDPETYFF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS: PR00237; GPCRRHODOPSN.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE: 347_AA; 39473_MW; F107488E57E025F1_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ptam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional admotation of a full-length mouse cDNA collection.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y
132 TTRPFKTSSPSNLLGAKILSVVIWAFMELISLPNMILTNRRPKDKDVTKCSFLKSEFGLV 191
                                                 126 TTEPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNROPRDKNVKKCSFLKSEFGLV 185
                                                                                                                                                                                                                             12 NTTESPGTSTLCVRDYKITQVLFPLLYTVLFFAGLITNSLAMRIFFQIRSKSNEIIFLKN 71
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                  6 NLISAFGNTSLCTFDYKITQVLFFLLYTVLFFVGLITNGLAMRIFFQIPSKSNFIIFLKN 65
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                                                                                                                   TVISULLMILTEPEKILSDAKLGAGPLRTLVCQVTSVTEYETMYISISELGLITIDRYLK 131
                                                                                                                                                                        TVISDLIMILTEPEKILSDAKIGTGPLETFYCQVTSVIFYPTMYISISFIGLITIDRYQK 125
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                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 1555.5; DB 11; Length 347; 88.7%; Pred No 2.7e-131;
                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
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01-MAR-2001 (TIEMBLIEL, 16, Created)
01-MAR-2001 (TIEMBLIEL, 17, Last segmence update)
01-JUN-2001 (TIEMBLIEL, 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21037966; PubMed=11196645;
Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,
Ramakrishnan V., Yang K.-B., Nurden P., Nurden A., Julius D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Rodentia; Seiurognathi; Muridae: Murinae: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POY12 PLATELET ADP PECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antithronbotic Drugs.",
Nature 409:202:207(2001),
EMBL; AF313450; AAG48945.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; INKOOC276; GPCR_Phodpsn
pfam; pF00001; 7tm_1; 1.
pRINTS; PR00237; GPCREHUDDOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of the Platelet ADP Receptor Targeted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 RNSLTSMLRCSNS-TSTSGTNKKKCQEGGEPSEETPM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 RNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 FICEVPERFARIPYTLSQTRAVEDCSAENTLEYVKESTLWETSLNACLDEFTYFFLCKSF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 FICEVPEHFARIPYTLSQTRDVFDCTAENTLEYVKESTLWLTSLNACLDFFIYFFLCKSF 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conley P.B.;
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                                                                                                                                                                                                 132 TTRPEKTSSPSNILJGAKILSVAIWAEMFILJSLPNMILTNRRPKDKDITKCSFLKSEFGLV 191
                                                            246 FICFVPFHFARIPYTLSOTRDVFDCTAENTLEYVKESTIMLTSINACIDEFTYFFICKSF 305
                                                                                                                                192 WHELVNYLCOVIEWINELIVIVOYSLITKELYRSYVETEGSAKAPKKRVNIKVEIIIAVE 251
                                                                                                                                                               186 WHEIVNYICQVIEWINELIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVE 245
                                                                                                                                                                                                                              126 TTRPFKTSNPKNLLGAKILSVVIWAEMELLSLPNMILTNROPRDKNVKKCSFLKSEFGLV 185
 312 RNSLMSMLRC----STSGANKKKGQEGGDPSEETPM 343
                                  306 RNSLISMLKCFNSATSLSQDNKKKEQDGGDPNEETPM 342
                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                   66 TVISDLLMILTEPPKILSDAKIGTGPLRTEVCQVISVIEVFTMVISISFIGLITIDHVOK 125
                                                                                                                                                                                                                                                                                                                                                                6 NUTSAPGNISLCTRDYKITQVLEFLLYTVLEFVGLITNGLAMPIFFQIRSKSNFIIFIKN 65
                                                                                                                                                                                                                                                                                                                                                                                                      293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA; 39047 MW; 7AEOAFCE66674136 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      86.0%; Score 1528.5; D
86.9%; Pred No. 6.9e-1
                                                                                                                                                                                                                                                                                                                                                                                                      , Pred. No. 6.9e-129;
17; Mismatches 22; Indels
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Best Local :
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Matches 155: Conservative
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Friam; PE00001; 7tm 1; 1.
PRINTS; PR00247; GPCRRHODOPSN.
PROSITE: PS00247; G PROTEIN_RECEP_F1 1; UNKNOWN_I.
PROSITE: PS00242; G_PECTEIN_RECEP_F1_2; I.
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01 JUN 2001 (TEMHEREL 17, Last sequence update)
01 JUN 2001 (TEMHEREL 17, Last sequence update)
01 JUN 2001 (TEMHEREL 19, Last annotation update)
01 JUN 2001 (TEMHEREL 19, Last sequence update)
01 JUN 2001 (TEMHEREL 19, Last sequence update)
01 JUN 2001 (TEMHEREL 19, Last sequence update)
01 JUN 2001 (TEMHEREL 17, LAST SEQUENCE U
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Lee D.K. Mrayer T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans I.E., George S.R., O'Dowd B.P.;
"Discovery and mapping of ten novel C protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wittenberger T., Schaller H.C., Hellebrand S.;
"An expressed sequence tag (est) data mining strategy succeeding in the discovery of new q-protein coupled receptors.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein coupled receptor.";
Submitted (FEB 2001) to the EMRL/GenBank/DDRT databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo
NCBI TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKSG/7 OR GPR85 OR GPR94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a Novel Human ADP Receptor Coupled to Gi.";
J. Biol. Chem. 276:41479:41485(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parmentier M., Boeynaems J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed 11546776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 275:83 91(2001).
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135 KPVFAKTVSTETWEFLEFTSLENMILSNKEATDSSVKKCASLKGPLGLKWHOMVNNICQF 194
                                                                    137 NILKIAKILSVVIWAFMFILSLPNMILTNROPRDKNVKKOSFLKSEFGLVWHEIVNYICOV 196
                                                                                                                                                                                                    77 FPEKILSDAKLATORDAKTEVOOVISVIFYFIMYISISFLALITIDAYOKTTRPEKTSNPK 136
                                                                                                                                                        75 LEFKILSDSHLAEWQLKAEVCKESSVIFYETMYVGIVLLGLIAEDRELKIIRPLRNIFLK 134
                                                                                                                                                                                                                                                                                                            15 CPROTRIVULVEPALYTVVELTGILLNTLALWVEVHIPSSSTEIIYLKNTLVADLIMTLM 74
                                                                                                                                                                                                                                                                                                                                                                                    17 CIRDYKITOVLEPILLYTVLEFVGLITNGLAMRIFFQIRSKSNFIIFLKNIVISDLLMILT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF345565; AAK29068.1;
AF295368; AAK01864.1;
AF411113; AAL26484.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conzalez N.S., Detheux M., Brezillon S., Lanney V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38440 MW; F234ABH50016DF34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.6%; Score 829; DB 4;
49.1%; Pred. No. 2.4e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 102;
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                                                                                                                                                                                 Matches 151;
                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                          PFAM, PF00001, 7tm.1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazca, Chordata, Craniata, Vertebrata, Eutereostomi;
Mammalia, Eutheria, Rudentia, Schurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD: MGI:1921441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21085660; PubMed-11217851;
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66 KNTLVADLIMALMLPFKILSDSHLAPWQLRGFVCTLSSVVFYETMYVGIMMLGLIAFDRF 125
                                          64 KNTVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVTSVIFYETMYISISELGLITIDRY 123
                                                                                                                                                                                                         Local Similarity
                                                                                     NTTGMQGENKSERCPRDTRMTQLLFPVLYTVVFLAGILLNTVALWVFVHIPSNSIFIVYL 65
                                                                                                                                  NLTSAPG--NTSLCTRDYKITQVLEPLLYTVLEFYGLITNGLAMRIFFQIRSKSNF11FL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSATSLSQDNRKKEQD 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK008013; BAB25409.1; -
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gpr86.
                                                                                                                                                                                                         44.78;
                                                                                                                                                                               63; Mismatches
                                                                                                                                                                                                    Score 794; DB 11;
Pred. No. 3.2e-63;
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Last annotation updat
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Best Local :
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01-MAR-2001 (TrEMBLIE). 16, Last sequence update)
01-JUN-2001 (TrEMBLIE). 17, Last annotation update)
7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           098866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1999) to the EMBI/GenBank/DDBJ databases EMBL: AF177211: AAG09275.1; ... InterPro: IPR000276: GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 OKTTRPFKTSNPKNLLGAKILSVVIWAFMELLSLPNMILTNRQPRDKNVKKCSFLKSEFG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "7 transmembrane G protein coupled receptor from hematopoietic
progenitors.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 LWWHQVVSHTCQLIEWAVFILMLLEYAVITKKVYNSYRKEBSKDS-RHKRLEVKVFIVMA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 LVWHFIVNYICOVIEWINELIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVEIIIA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PRO0237; GPCRRHODOPSN PROSITE; PS50262; C_PROTEIN_R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCHI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 VEFVCEAPLHEVRIPYTYSQTTNKTDCKLENQLFlAKEATLFLATTNICMDPLIYILLCK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 VFFICEVPEHEARIPYTLSQTRDVEDCTAENTLEVVKESTLMLTSLNACLDPFIYEFICK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piam; PF00001: 7tm 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 KETQKVPCVRWGKARTAGSSEDHHSSQTD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 SFRNSLISMLKCPNSATSLSQDNRKKEQD 332
                                                                                                                                                                                                                                  121 YKIVKPILTSIVQSVNYSKILSVLVWMLMILLLAVPNIILTNQGVKEVTKIQCMELKNELG 180
                                                                                                                                                     181 RKWHKASNYIFYSIFWYYFILLLYFYTAITRKIFKSHLKSRKNSTSVKRKSSRNIFSIVI. 240
                                                                                                                                                                                                                                                                      124 OKTTRPFKTSNPKNILLCAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFG 183
                                                                                                                   244
                                                                                                                                                                                           184 LVWHEIVNYICOVIEWINFLIVIVCYTLITKELYPSYVRTROVGKVPRKKVNVKVFIIIA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 41.7%; Score 741.5; DH 1
Local Similarity 44.1%; Pred No 1 66-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
301 PEREVLNKKLHMSLKVQN---DLEVSKTKRE 328
                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                     64 KNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRY 123
                                                                                                                                                                                                                                                                                                                                                                                             1 MNNSTTIDPPNOPCSWNWLITKQIIPVLYGMVFITGLLLNGISGWIFFYVPSSKSFIIYL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VUNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFL 63
                                                                                                                                                                                                                                                                                                                 KNIVVADELMALTEPEKVLADSALAPWQVNVEVCRVSAVIEYVNMYVSIVEEGLISEDRY 120
                                                                          VEVVCEVEYHIARIEYTKSQTEGHYSCETKETLLYAKEFTLLISAANVCLDEIIYEFICQ 300
                                                                                                              VPF1CFVPFHFAR1PYTLSOTBDVFDCTAENTLFYVKESTLWLTSLNACLDPF1YFF1CK 303
                                      SFR---NSLISM-LKCPNSATSLSQDNRKKE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scadden D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 AA; 38861 MW; 4376B50622A68A4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69, Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
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82F96Q
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RR OCC OCS PE
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                                                                                                                                                                                                                                                                                                                      RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96J78;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last sentence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
01-DEC-2001 (TrEMBLrel 19, Last sentence update)
CDMA FLJ14878 FIS, CLONE PLACETON 2348. WEAKLY SIMILAR TO PROBABLE
G PROTEIN-COUPLED RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sudano S., Shiratori A., Sudo H., Suqawara M., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Suqawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiquchi S., Watanabe S., Kimura K., Murakawa K., Ono Y., Takiquchi S., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Saito K., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96JZ8
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Mammalia; Eutheria; Primates; Cutarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                              Ol-JUN-2001 (TERMBLIEL. 17, Cheated)
Ol-JUN-2001 (TERMBLIEL. 17, Last sequence update)
Ol-DEC-2001 (TERMBLIEL. 19, Last annotation update)
ORDHAN G PROTEIN-COUPLED RECEPTOR 87.
                                                                                                                                                                                                                                                                         Q9BY21
                                                                    Eukaryota; Metazoa; Chordata; Craniata; verceordeo, Poseco
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 KVVKPFGDSRMYNITETKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 KTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGL 184
  SEQUENCE FROM N.A
                                         NCBI_TaxID=9606;
                                                                                                                 Homo sapiens (Human)
                                                                                                                                       GPR87 OF GPR35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 KWHTAVIYVNSCLEVAVLVILIGIYIAISRYIHKS -SPQFISQSSRKPKHNQSIRVVVA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 VWHEIVNYLCQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRK-KVNVKVFIIIA 243
                                                                                                                                                                                                                                                                                                                                                                                        320 SESRRLEKKSNIPTPSESIPSLOSVRRSE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                  304 SERNSLI - SMLKCPNSATSLSQDNEKKE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 VEFTCELPYHLCRIPFTESHLDRLLDESAOKILYYCKELTLELSACNVCLDP11YFFMCR 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 VFFICEVPFHEARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 NIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDKYL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 NTVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVTSVIFYFTMYISISELGLITIDRYO 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 NRSDGPGKNTTL---HNEEDTIVLFYLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.3%; Score 699.5; DB 4; Length 358; illarity 42.6%; pred. No. 9.6e-55; Conservative 67; Mismatches 113; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                              PPELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41462 MW; 7822700C8FRCC7F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                 PRT;
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RESULT 11
QUARTY
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                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN 2001 (TrEMBLIEL 17, Created)
01-JUN 2001 (TrEMBLIEL 17, Last sequence update)
01-JEC 2001 (TrEMBLIEL 19, Last annotation updat
                                    MEDIINF.21172992: PubMed 11273702:
Wittenberger F., Schaller H.C., Heliebrand S.
                                                                                                                                                                                                                                                                    Bukaryota: Metazoa:
                                                                                                                                                                                                                                                                                                                                                                                               G PROTEIN COUPLED RECEPTOR GPR87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99MT7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              099MT7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00247: G PROTEIN_RECEP_F1_1: 1. PROSITE: PS00262: G PROTEIN_RECEP_F1_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMIST.
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI FaxID 10090;
                                                                                                                                                                                                                                    Mammalia: Butheria: Rodentia:
                                                                                                                                                                                                                                                                                                                 Mus musculus (Monse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINIS;
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Lewis T., Evans J.F., George S.R., O'bowd H.F.;
"Discovery and mapping of ten novel G protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDIJINE 21458557; Pubmod 11574155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An expressed sequence tay (est) data mining strategy succeeding the discovery of new q protein coupled receptors.";
J. Mol. Biol. 307:799-813(2001).
"An expressed sequence tag (est) data mining strategy succeeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 275,83 91(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 VEFTCELFYBLCKIPETESHLDRLLDESAQKILYYCKETTLELSACNVCLDPTTYFFMCR 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 KITEPEKISNEKNITGAMITSVVIWAFMELLSLENMILINEQERDKNYKKOSELKSEFGE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VWHELVNYLOOVIEWINELLVIVOYELITKELYKSYVRIRGVGKVPRK-KVNVKVELLIA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (20 SESRRIPKKSNIPTRSESIPSIQSVPRSE (48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *04 SERNSI I - SMI KOPNSATSI SQDNPKKE - 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 VEFICEVPEHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCK 303
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SIMILARITY: HELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS.
IL: AF237763; AAKO1858.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWHTAVTYVNSCLEVAVLVILIGCYIAISPYTHKS -SPQFISQSSFKFKHNQSIRVVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVVKFFGFSFMYSTIFTKVLSV/VWVIMAVLSLFNIILINGQFTEDNIHESKLKSPLGV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIVVADLIMILIEPERIVEDAGEGEWYFKFILCKYTSVLEYANMYISIVELGLISIDRYL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTVISHLIMILTEPEKII SHAKI GTGPLETEVOQVTSVIEYETMYISISELGI.ITIDEYQ 124
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                                                                                                                                                                                                                                                                    Chordata; Cramiata; Vertebrata; Euteleostomi;
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68; Mismatches 11s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                    Schuroquathi, Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                        Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cymomolqus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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PFINTS: PR00237: GFCREHODOPSN.

PROSITE: PS00237: G_PROTEIN_RECEP_F1_1; 1.

PROSITE: PS00267: G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor. Glycopiotein; Receptor; Transmembrane SEQUENCE 359 AA; 41462 MW; 2EB313C273EFCDEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the discovery of new g-protein coupled receptors.";

J. Mol. Biol. 307:799-813(2001).

-!- SUBCELULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)

-!- SUBCELULIAR CONTROL OF FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF29-366; AAKO18-66.1; -.
                    PRINTS: PRO0237: GPCRRHODOPSN.

PROSITE: PS00237: G_PROTEIN_PECEP_E1_1: UNKNOWN_1
PROSITE: PS50260: G_FROTEIN_RECEP_E1_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TERMHITEL 17, Created)
01-JUN-2001 (TERMHITEL 17, Last sequence update)
01-DEC-2001 (TERMBLEEL 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BE53
  SEQUENCE
                                                                                     InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                Submitted (MAP-2001) to the EMRL/GenBank/DDBJ databases EMBL: AB056816; BAB39342.1; -.
                                                                                                                                                                          libraries."
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9541;
                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BE53;
                                                                                                                                                                                                                                                             TISSUE-FRONTAL CORTEX;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 RRIFKKSNIRTRSESIRSLQSVRRSE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 NSLI -- SMLKCPNSATSLSQDNRKKE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 TOFLPYHLORIPFIESNIDRILDESAHKILYYCKEMTIFISACNVOLDPILYFEMCKSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 ICEVPEHFAKTPYTLSÖTKDVEDCTAENTLEYVKESTLWLISLNACLDPETYFETLCKSER 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 MAVTYVDSCLEVAVLVILIGCYIAISRYIHKS--SRQFISQSSRKRKHNQSIRVVVAVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 ETANY LOQVIEWINELI V EVOYEL LEKELYRSYVEERGVGKVERK-KVNVKVELL LAVEE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 KPFGDSRMYSTTFTKVLSVCVWVIMAILSLPNITLTNGQPTKENIHDCMKLKSPLGAKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 RPEKTSNEKNLIGAKILSVVIWAEMELLSLENMILTNEGERDKNVKKCSFLKSEEGLVWH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hes 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ISDLLMINTEPEKILSDAKLGTGPLRTEVCQVTSVIFYFTMYISISFLGLITTIDRYQKIT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 STSEGHGKNSTLHNKFDTIILPVLYLVIFVASILLNGLAVWIFFHIKNKTSFIFYLKNIV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TSAPGNISLOTEDYKITQVLEPILLYIVLEFYGLITNGLAMKIFFOLESKSNELLELKNIV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.6%; Score 685.5;
41.7%; Pred. No. 1.
  26356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65; Mismatches 120;
  47907F5DBEEDD22C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228
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Query Match

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                                                                                                                                                     Matches
                                                                                                                                                                         Best
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                       SUDDITTED (JUN-2001) to the EMBL/GenHank/DDBJ databases.
-!- SUBKCELLULAR LOCATION- INFECRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS IO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: AF345566: AAK93069 1.
EMBL: BC009540: AAK93069 1.
IN-PAPO: IPROD0276 GPCE_Phodpsn
Pfam: IPV00001; 7tm.1: 1.
PKINTS: PR00237; GPCKRHODOPSN.
PROSITE: PR00237; GPCKRHODOPSN.
PROSITE: PS50262; G_PRCTEIN_RECEP_F1_1; 1.
PROSITE: PS50262; G_PRCTEIN_RECEP_F1_2; 1.
G-PCOLEIN coupled receptor: Glycoprotein; Receptor: Transmembrane.
G-PCOLEIN coupled receptor: Glycoprotein; Receptor: Transmembrane.
SEQUENCE 269 AA: 31443 MM: 1E7D49REE20717F6 CPC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wand Y.-9, Gond L.;
"Identification of FKSHTR, a novel gene encoding a putative G-protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Eutel
Mammalia: Eutheria: Primates; Catarrhini: Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/OrnHank/Sobbl databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG78 (G PROTEIN-COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BXC2;
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                                  133 SNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RKNNKKLEGKVFVVVAVFFVCFAPFHFTRVPYTYSQTNNKTIN'RLQNQLF1AKETTLFLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 KVPRKKVNVKVFILLAVFFLCFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLMLT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 RDKNVKKCSFLKSEFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 MYTSISFLGLITIDRYOKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AINICMDPLIYIFLCKKETEKLECMRGRKTIAS--SÜENÜSSÜTD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 SINACIDPETYEFICKSERNSLISMIKERNSALSISCONRKKEGE 322
61 SRMYSITETKVI.SVCVWVIMAVI.SI.PNIII.TNGQPTEDNIHDCSKI.KSPI.GVKWHTAVTY 120
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TPSSVKKCASLKGPLGLKWHOIVNNISQFIFWTVFVLMLVFYVVIAKKVYDSYRKSKSKD 120
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                                                                          MTLTEPERIOHDAGEGRWEEKFILGRYESVLEYANMYTSIVELGLISIDRYLKOVKREGD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                 31.1%; Score 553.5;
42.5%; Pred. No. 8.1
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                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence update)
                                                                                                                                                   No. 8.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AA
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01 MAY 2000 (TrEMBLITEL 13, Created)
01 MAE 2001 (TrEMBLITEL 16, Last sequence update)
01-DEC-2001 (TrEMBLITEL 19, Last annotation update)

PLATELET-ACTIVATING FACTOR RECEPTOR

Q9TTY5; 9 A.L.L.60

PRELIMINARY;

PRT;

Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

SEQUENCE FROM N.A

NCBI\_TaxID=9913; Bovidae; Bovinae; Bos

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"Molecular cloning of a probable G protein-coupled receptor with three transmembrane domains.";
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01-JUN-2001 (TrEMBLITEL 17, Last sequence update)
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PUTATIVE G PROTEIN-COMPLED RECEPTOR GPCR1.
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PPINTS; PR00237; GPCPPHODOPSN
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Matches 101; Conservative 63; Mismatches 136; Indels 31; Gaps
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PRINTS; PRODUZ17; GPCRRHOPOPSN.
PROSITE: PSOUZ17; G_PROTEIN_RECEP_F1 1; UNKNOWN_1.
PROSITE: PSOUZ62; G_PROTEIN_RECEP_F1_2; 1.
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Her H., Toemann U., Kanitz W., Wolkard R., Laurent P., Schwerin M.
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## SUMMARIES

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LSE_NEG.  Glycoprotein. (POTENTIAL).  POTENTIAL).  (POTENTIAL).  POTENTIAL).	This SWISS-PROT entry is copyright. It is produced through a ceilaboration between the SWISS Institute of Bioinformatics and the IMML outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is it no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb/sib/dp.anhounce/or send an email to license@isb-sib/sb).	warabayasi Y., atta S.; fed buman genes. 1. (AAAAAA) deduced by uman immatture myeloid tein. N COUPLED RECEPTORS.	ta; Eureleostomi; dae; Homo.		P33535 rattus Horv P29755 mus museculu Q9jhq3 rattus norv Q63645 rattus norv P35414 homo sapien Q95247 sus serota Q35210 meriones un P79350 bos taurus GUB675 mus museculu P32303 xenopus lae P35373 xenopus lae P35373 xenopus lae

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Seprotein coupled receptor: Transmembrane; Glycoprotein
                              PROSTIE: PS00237; G_PROTEIN_RECEP_FI_1; FALSE_NEG, PROSTIE: PS50262; G_PROTEIN_RECEP_FI_2; 1.
                                                                                                     Ptam; PF00001; 7tm,1;
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or send an email to license-lisb sib.ch).
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Chartton M.E., Williams A.S., Fogliano M., Sweetnam P.M.
Submitted (OCT 1996) to the EMBL/GenBank/DDBJ databases
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15.000 1998 (Rel. 36, Last annotation opdate)
Probable 6 protein coupled receptor VTR 15-20.
Reatins not regions (Rat).
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                                                                                                                                InterPro: IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                    EMBL: 076206; AAB71745.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNTION: ORPHAN RETEPTOR.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIBLEARITY: HETONGS TO FAMILY 1 OF C-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECHENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 REILOKKLHIPLKA 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 FVCFVPYHIAKIPYIKSQIEAHYSCQSKEILKYMKEETILLSAANVCIDPITYFFLCQPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 WHEASHYTEVALEWIVELLLIVEYTAITKETEKSHLESSPISTSVEKKKSSRNIFSIVEVE
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Pred. No. 3.4e-45
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CYTOPLASMIC (POTENTIAL).

N LINKED (GLCNAC. . .) (
N LINKED (GLCNAC. . .)
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7 (POTENTIAL).
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Best Local :
                                                                 TISSUE-Peripheral blood monocytes:
MEDILINE-9803661; PubMed-9370294;
Jacobs K.A., Collins-Racie L.A., Colbert M., Duckert M.,
Golden-Fleet M., Kelleher K., Kriz R., LaVallie E.R., Merberg D.,
Spaulding V., Slover J., Williamson M.J., McCoy T.M.;
"A genetic selection for isolating cDNAs encoding secreted proteins.
Gene 198:289-296(1997).
-i- PINCTION: ORPHAN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                 Homo sapiens (Human)
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30-MAY-2000 (Rel. 39, Last sequence update)
16-QCT-2001 (Rel 40, Last anotation update)
Probable G protein-coupled receptor H963.
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           This SWISS PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                        Eukaryöta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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N-LINKED (GLONAC. . .) (F
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EXTRACELLULAR (POTENTIAL)
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EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO0237; GPCHRHOPOPSN
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1
PROSITE; PS50262; G_PROTEIN_PECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                    Probable G protein-coupled receptor GPR34.
                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                              GPRY_MOUSE
                                                                                                GPR34
                                                                                                                                                                                                                                                Q9R1Kb;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 FKISNEKNILGAKILSVVIWAFMFILISLENMII TNEQDEDKNVKKCSFILKSEFGLVWHEI 189
                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 CEVPYHIVRIPYTLSQTEVITDCSTRISLEKAKEATLLLAVSNLCEDPILYYHLSKAFRS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 CFVPFHFARIPYTI.SQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFI.CKSFRN 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 VNYICGVIEWINE LIVIVCYTLITKELYPSYVRTPGVGKVPR-KKVNVKVFIIIAVEFI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 CKTYRIQEPGFAKMISTYVWLMYLLIMYPNMMIPTKDIKEKSNYGCMEFKKEFGRNWHLL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                    295 KVTETFASPKETKAQKEKLRCENNA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 St.1------SMLKCPNSA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LITLALPVKIVVD--LGVAPWKLKIFHCQVTACLIYINMYLSIIFLAFVSIDRCLQLTHS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 NTSLCTRDYKITOVLFPLLYTVLFFVGLITNGLAMPIFFQIRSKSNET-IFLKNTVISDL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 LMILTEPEKILSDAKIGIGP- LRTEVCQVTSVIFYETMYISISFLGLITTIDRYQKTTRP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NSSPECTVYKDLED-FTYFFYLVFLVGLIGSCFATWAFIQKNTNHRCVSLYLINLLTADF 61
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2 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99326137; PubMed=10395919;
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PRINTS; PR00237; GPCPRHODDPSN.

PROSITE; PS00237; GPCPRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

Receptor, G_PROTEIN_RECEP_F1_2; Transceptor; Transce
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-I TISSUE SPECIFICITY: BROADLY EXPRESSED.
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203 RHNAKGEAIFNFYLVVMFWLIFLLIILSYIKIGKNLLRISKRRSKFPNSGKYATTARN--
                                                                181 EFGLYMHEIVNYICOVIFMINFLIVIVCYTLITKELYR-SYVRTR--GVGKVPRKKVNVK 237
                                                                                                                                                                                                            121 DRYQKTTKEFKTSNEKNILIGAKILSVVIWAFMFILSLFNMILTNEQPPDFNVKKYSFIKS 180
                                                                                                                                                                                                                                                                                                                                                61 IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI 120
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                                                                                                                                                                                                                                                                            84 TYLLNVAVADLLLIECLPERIMYHINONKWTLGVILGKVVGTLEYMNMYISIILLGEISL 143
                                                                                                                                                                                                                                                                                                                                                                                                                    25 WASWNESGVENVIS CPMDEKLLSTVLTTFYSVIFLVGLVGNITALYVFLGIHRKRNSIO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QAVDNI/TSAPGNTSI/CTRDYKITQVLFPLLYTVI/FFVGI/TINGIAMRIFFQIRSKSNFI: 60
                                                                                                                                        DRYIKINRSIQQRPAITTKQSIYVCCIVWT-VALAGFLTMIILTLKKGGHNSTMCFHYRD 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.1%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Mismatches 154;
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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Pred. No. 4.8e
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; G04E1ClAS2521045 CRC64;
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N-LINKED (GLCNAC. ...)
N-LINKED (GLCNAC. ...)
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                                                                                                                                                                                                                                                                                                                                                                     TISSHE-Placenta:
Isoda T., eta i., Hayashi K., Suqiyama T., etsuki T., Suzuki Y., Nishikawa T., eta i., Kayashi K., Suqiyama T., Takahashi Fujii A., Hara H., Nishikawa T., Nomura Y., Toqiya S., Komai T., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saite K., Yamamoto J., Wakamatshi A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
"NEIxe human cDNA sequencing project.";
Submitted (MAY 2001) to the EMHL/GenHank/DDHJ databases.
                                                                                                                                                                                          This SWISS PROLEETLY is copyright. It is produced through a collaboration between the Swiss Institute of High Indition and the EMHL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way.
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16 % 2001 (Rel. 40, Last sequence update)
16 % 2002 (Rel. 41, Last annotation update)
01 MAR 2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                        modified and this statement is not removed.
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Schoneberg I., Scholz A., Grosse R.,
Schultz G., Gudermann T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutberia: Primates: Catarrhini: Hominidae: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                               or send an email to license dish sib.ch)
                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condenital stationary night blindness type 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marchese A., Sawzdargo M., Nguyen T., Cheng R., Heng H.H., Nowak T., Im D. S., Lynch K.R., George S.R., O'Dowd B.F.;
"Discovery of three novel orphan G-protein-coupled receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel subgroup of class I G protein coupled receptors."; Biochim. Biophys. Acta 1446:57-70(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Physical mapping and exclusion of GPR34 as the causative gene for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacobi F.K., Broghammer M., Pesch K., Zrenner E., Berger W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20434921; PubMed-10982042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 : SIMCELLULAR INCATION: Integral membrane protein (By similarity) in TISSUE SPECIFICITY: REGADLY EXPRESSED.
SIMILARITY: RELONGS TO FAMILY L OF G-PROTEIN COUPLED RECEPTORS.
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                                         AK027780; BAB55362.1;
                                                                    AF118670;
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1PR000276; GPCR_Rhodpsn
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                                                                                    AAD50541.1;
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                                                                                                                                                    moved. Usage by and for commercial (See http://www.isb-sib-ch/annonner/
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ROCCOS GENERAL

PTAFR OR PAFR.

Homo sapiens (Human) Eukaryota; Metazoa;

NCBI\_Tax1D=9606;

Mammalia; Eutheria; Primates; Catarrhini;

Chordata; Craniata; Vertebrata; Euteleostomi;

Hominidae;

01-MAY-1992 (Rel. 22) Created) 01-MAY-1992 (Rel. 22) Last sequence update) 16-007-2001 (Rel. 40) Last annotation updat

16:007:2001 (Rel. 40, last unretation update) Platelet activating factor receptor (PAF-R).

PAFR\_HUMAN RESULT

P25105 PAFK\_HUMAN

STANDARD;

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PRINTS; PR00237; GPCRKHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTFIN_PECEP_F1_2; 1.
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                                                                                                       210 KHNAKGEALENELLVVMEWLIPILLILLSYLKIGKNILKISKRRSKEDNSGKYATTARN-
327 YFLMSSNIRKIMCQLL 342
                          298 YFFLCKSFRNSLISML 313
                                                 268 SFIVLIIFTICFVPYHAFRFIYISSQL-NVSSCYWKEIVHKTNEIMLVLSSFNSCLDFVM
                                                                            238 VFIIIAVFFIGEVPFHFARIPYILSQIRDVFDCTAENTLFYVKESTLWLTSLNACLDPFI
                                                                                                                                 181 EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYR-SYVRTR--GVGKVPRKKVNVK
                                                                                                                                                            151 DRYIKINRSIQQRKAITTKQSIYVCCIVW-MLALGGFLTMIILTLKKGGHNSTMCFHYRD 209
                                                                                                                                                                                     121 DRYQKTTRPFKTSNPKNILGAKILSVVIWAFMFILLSLPNMILTNRQPRDKNVKKCSFLKS 180
                                                                                                                                                                                                                91 IYLLNVAIADLLLIFCLPFRIMYHINQNKWTLGVILCKVVGTLFYMNMYISIILLGFISL 150
                                                                                                                                                                                                                                                                   32 QPPQNESATP-NYTTCPMDEKLLSTYLTTSYSVIFIVGLYGNIIALYVFLGIHRKRNSIQ 90
                                                                                                                                                                                                                                                                                           2 QAVDNLTSAFGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI: 60
                                                                                                                                                                                                                                        IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI 120
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N-LINKED (GLONAC. . .)
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REPORT OF A PROPERTY OF A PROP
SEQUENCE FROM N.A.

MEDILINE-92028922; PubMod-1656963:
Ye P D . Prossnitz E.R., Zou A., Cochrane C.G.;
"Characterization of a human cDNA that encodes a functional receptor for platelet activating factor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 180:105-111(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and characterization of the platelet-activating factor receptor gene expressed in the human heart."; Biochem. Biophys. Res. Commun. 189\cdot617-624(1992).
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J. Biol. Chem. 267:9101-9106(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of a human platelet-activating factor receptor gene:
evidence for an intron in the 5'-untranslated region.";
Am. J. Respir. Cell Mcl. Hiel R.248.244(1993).
1. FUNCTION: RECEPTOR FOR FLATELET ACTIVATING FACTOP, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A 3 PROTEIN THAT ACTIVATY A PHOSPHATIDYLINOSITOL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93112021, FubMed-1281995;
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Submitted (XXX:1992) to the EMHI/GenHank/DDRJ databases
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                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation between the Swiss institute of Bioinformatics are no restrictions on its the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                      or send an email to license lisb-sib.ch)
                                                             EMBL:
                                                                                                                                                                                     емві; м80436;
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                              M88177;
S52624,
L07334;
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   S56396;
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AAB24695.2; -.
AAA60108.1; -.
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BAA@1@50.1;
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Best Local Similarity
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GCRDb: GCR_0285; --
GCRDb: GCR_0414; --
GCRDb: GCR_0478; --
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pr0SITE; ps00237; G_PPUTEIN_RECEP_F1_1, 1.
pr0SITE, ps50252, 3_pputein_recep_F1_2; 1.
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                    240 IIIAVEFICEVPEHEAPIPYTLSQSKUVFUCTAENTLEYVKESTLWLTSLNACLDPFIYE 299
                                                               180 SEFGLVMHEIVNYTCQVIFMINEL:VIVCYTI ITWELYRSVVRTRGVGKVPRKKVNVKVF 239
                                                                                     121 RPIKTAQANTKKRGISLSLVIWVAIVGAASYFLILDS: TNTVPDSAGSGNVTPC-FEH 176
                                                                                                                              61 MAUMLETLITLPHWIVYYQNQGNWILPKELCNVAGC! FFINTYGSVAFIGVITYNRFUAVT 120
                                                                                                                                                  68 ISDLLMILTEPEKILSDAKLGTGELRTFVCQVTSVIEYFTMYISISFIGLITIDPYOKTT 127
                                                                                                                                                                                               11 PGNTSLCTRDYKITQVLEPLLYTVLEFVGLITNGLAMRIFFOLR--SKSNFI-IFIKNIV 67
                                                                                                                                                                          3 PHDSSHMDSEFRYT--LFPIVYSIIFVLGVIANGYVI.WVFARI.YPCKKFNEIKIFMVNI/T 60
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                                          YEKGSVPVLLIHIFIVFSFFLVFLLILFCNLVİIRTLLMQPVQQQRNAEVKRALMM-VC
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K -> N (IN REF. 5).
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N -> S (IN DBSNP:
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HODda Z. L. Nakamura M., Miki L., Minami M., Watanabe T., Seyama Y., okado H., Toh H., Ito K., Miyamoto T., Shimizu T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryotu: Metazoa: Chordata: Craniata: Vertei
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01 AUG 1991 (Rel. 19, Last sequence up
01 OCT 1996 (Rel. 34, Last annotation
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: RELONGS TO FAMILY 1 OF G-PROTEIN COUPLED PECEPTORS
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MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
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                                                                                                                                                                                                                                                                                                                                                             *Epstein-Barr virus induced genes; first lymphocyte-specific g-
protein coupled peptide receptors.*;
J. Virol. 67:2200-2220(193).
-1- FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS
LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-93188173; PubMed-8383238;
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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16-OCT-2001 (Rel. 40, last annotation update)
E----
                                                                            EMBL; 1.08177; AAA35924.1;
                                                                                                                     or send an email to licensewish-sib.ch).
                                                                                                                                    entities requires a license agreement (See http://www.isb-sir-ch/comeconses)
                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kieff E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                CAUTION, IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR
                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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PIR; B45680; B456 GCRDb; GCP\_0499;

B45680.

MIM; 605741;

PRINTS;

PR00237;

GPCRRHODOPSN

Pfam; PF00001; 7tm\_1;

InterPro: IPR000276; GPCR\_Rhodpsn

PS00237,

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                                                                                                                                                                               01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cystedayl leaket; lene receptor 2 (CystTR2).
CYSTTR2 OR CYSTT2.
Sus scrofa (Piq).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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SEQUENCE : Takasu...
Kamohara M., Takasu...
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                                                                                                                                    Mammalia: Entheria: Cetartiodartyla: Suina:
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                                        Takasaki J., Matsumoto M., Matsumoto S., Saito
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                    Matsushime
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EXTRACELULAR (POTENTIAL)
7 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                         Craniata, Vertebrata, Euteleostomi;
Jartyla; Suina; Suidar; Sus
                                                                                                                                                                                                                                                                                                                                                         PRT:
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                    H., Furuichi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2000) to the EMBL/GerBack/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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    -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN CONFLET RECEPTORS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                            188
                                                                                                                                                                                            130
                                                                                                                                                                                                                           115 LGLITIDRYOKTTRPFKTSNPKNILIGAKILISVVIWAFMFILISLPNMILITNROPRDKNVKK 174
302 NFFLYYFAGENFKDRLKSALR 322
                             294 DPFIYFFLCKSFRNSLISMLK 314
                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                          17 MEPNSTLGNHNSNRSCTTENFK -- REFYPIVYLVIFIWGALGNGFSIYVFLKPYKKSTSV
                                                                                                                                                                                                                                                                                           61 -IFLKNTVISDLLMILTFPFKI-----LSDAKLGTGPLRTFVCQVTSVIFYFTMYISISF 114
                                                                                                                                                                                                                                                                                                                                                         1 MQAVDNLTSAPGNTSLCTRDYKITQVLFPILLYTVLFFVGLLTNGLAMRIFFGIRSKSNF1 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Receptor for cysteinyl lenkotrienes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calcium second messenger system (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mediated via a G-protein that activates a phosphatidylinositol
                                                                                             VNVKVETITAVEETCEVEEHEARTEYELSQTPEVEGGTAENTLEYVKESTLWLTSLNAGT 293
                                                              ALITVITALITELLCFLPYHVLRTLHLLEWKAD---
                                                                                                                            CLELNSN-KVTKLKTMNYVALVVGFVLPFGTLSTCYLLTTRALLKVEVPESGL-KLSHRK
                                                                                                                                                           CSPLKSEFCLVWHETVNYTCQVT-FWTNFLTVTVCYTLTTKELYRSYVETECVGKVPRFE
                                                                                                                                                                                          LTVLSVVRFLATVHPFRLHTTSIKNAWILGGVIW--IFIMASSTVLLKNGSEGKDNVTL 187
                                                                                                                                                                                                                                                            NVFMLNLAISDLIFTITLPFRVDYYLKGSNX1FGDTP-----CRIMSYSMYVNMYSSIYF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coupled receptor; Transmembrane; Glycoproterr 1 43 EXTRACELLULAR (POTENTIAL).
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345 AA:
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206
227
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345
188
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177
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                                                                                                                                                                                                                                                                                                                                                                                                       20.6%; Score 367; DB 1; 29.0%; Pred No. 4 3e-18;
                                                                                                                                                                                                                                                                                                                                                                                    72, Mismatches
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N-IINKED (GLONAC ) (POT
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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4 (POTENTIAL)
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                               -KCKDRLHKAVAVTLALAAANSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                          Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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  Querry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosomal localization and up-regulation of expression by lipopolysaccharide in peritoneal resident macrophages."; Hoothem, 1 414:671-678(1996).
                                                                                                  CARBOHYD
                                                                                                                                         NIVM
                                                                                                                                                                                                                                                                                                                                                                                NIAMOG
                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemotaxio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein compled receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSTIE: PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSTIE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PROLISE: PAFRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000276; GPCK_Rhodpsn. Pram: PF00001: 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGT:108066; Ptatr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or Send an email to licensesisb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics, and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noma M., Shimizu T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL 1998 (Rel. 46, Created)
15-JUL 1998 (Rel. 46, Last sequence update)
15-JUL 1998 (Rel. 46, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE 96239129; PubMed 8670084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN 129/SV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI Tax10: 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Platelet activating tactor receptor (PAF R)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A murine platelet activating factor receptor gene: cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELULAR LOCATION: Integral membrane protein.
SIMILARITY: HELONIS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCR 1618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsuda Y., Nakamura M., Waqa I., Kume K., Izumi T.,
                                                                                                                                                                                                                                      114
134
156
185
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205
233
233
254
275
275
241
                                                                                                                                                                                                                                                                             39148 MW;
    20.6%:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein,
                                                                                        CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
  Score 366;
                                                                              BY SIMILARITY
                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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                                                           CAA8CDDBD8D26897 CRC64;
                                                                                                                                                                                                                                        (POTENTIAL)
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  DH 1;
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Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P46002;
Ol-NOV-1995 (Rel. 32, Created)
Ol-NOV-1995 (Rel. 32, Last sequence update)
Ol-OCT-1996 (Rel. 34, Last annotation update)
Platelet activating factor receptor (PAF-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             platelet-activating-factor-receptor cDNA.";
Eur. J. Biochem. 221:211-218(1994).
-i- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOIACTIC
                                                                                                                                                                                       use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Spicen; MEDLINE-94222063; PubMed*8168510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata,
Mammalia; Eutheria; Rodentia;
                  Pfam; PF00001; 7tm_1; 1.
PRINTS; PR01153; PAFRECEPTOR
                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation

    SUBCELLULAR LOCATION: Integral membrane protein.
    TISSUE SPECIFICITY: PRESENT IN ALMOST ALL ORGANS INCLUDING SPIEEN,
SMALL INTESTIBE, KIDNEY, LUNG, LIVER AND BRAIN
    SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bito H., Honda Z., Nakamura M., Shimizu T.; "Cloning, expression and tissue distribution of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAFR_RAT
                                                        InterPro; IPRüüüz7k; GPCR_Rhodpsn
                                                                               GCRDb; GCR_0985;
                                                                                                     EMBL; U04740; AAA18422.1;
                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                       entities requires à license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 CEVPHHVVQLPWTLAELG--YQTNFHQAINDAHQITLCLLSTNCVLDPVIYCFLTKKFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 CEVPEHEARIPYTLSQTRDVEDCTAENTLEYVKESTLWLTSLNACLDPETYEELCKSERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 FTAFCFFLVFFLTFYCNLVTTHTLLTQPMRQQ--RKAGV----KRRALWMVCTVLAVFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 TRKRGISLSLIIWVSIVATASYFLATDSTNLVPNKDGSGNITRCFEHYEPYSVPILVVHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 DYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLLMILT
                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                              CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SLISMLKCPNSATS 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata, Craniata, Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1

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Best Local
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DOMAIN
SEQUENTE FROM N A
TISSUE-T-cell;
MEDLINE-9329058; PubMed-8393036;
Kaplan M.H., Smith D.I., Sundick R.S.;
"Identification of a G protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISHLFID
SEQUENCE
                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2Y_guilhoceptor 5 (F2Y5) (Furinciple receptor 5) (6Hl).
                                                                                                                                                                                                                    P2Y5_CHICK
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                                                                                                                               Gallus gallus (Chicken)
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                                                                              NCHI_TaxID=9031;
                                                                                                      Archosauria; Aves, Necquathae,
                                                                                                                Eukaryota: Metazoa: Chordala: Craniala, Vertebrala, Euleleosiomi,
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

RY SIMILARITY
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Pred. No. 9.1e-18;
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7 (POTENTIAL)
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  coupled receptor induced in activated
                                                                                                      Galliformes, Phasianidae, Phasianinae,
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Riginformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: INDUCED IN ACTIVATED 1-CELLS.
-!- SIMILARITY: MELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKIN'S; PKU1067; PZY5PRNOCPTR.

PRINTS; PRO1157; PZPHRNOCPTP.

FK-SITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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HSSP; P34996; 1DDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to licensemisb-sib ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL 62
                                                                                                                          FVPFHFARIPYTLSQTRDVFDC---TAENTLFYVKESTLWLTSLNACLDPFIYFF 300
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                                                                                                                                                                                                                                                                                                                                                                           FVFTLPFRIYYEV-VRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS
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5 (POTENTIAL)
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7 (POTENTIAL)
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RENEW RENEW SOUND FOR THE PROPERTY OF THE PRO
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Q9NS75 Q9B
                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
EMBL: AR038269; BAR03601.1;
EMBL: AF254664; AA017281.1;
                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license isb sib.ch).
                                                                                                                                                                                                                                                                                                                                                  This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation -
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Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR 2002 (Ref. 41, Last sequence update)
01-MAR 2002 (Ref. 41, Last annotation update)
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Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
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Mol. Pharmacol. 58:1601-1608(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heart, placenta, spleen, peripheral blood leukocytes and adrenal dland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.
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SUBSTELLHLAR LOCALION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed, with highest levels in the
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Xenopus laevis (African clawed frog)
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01-NOV-1997 (Rel.
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EMBL; AB041644; BAB16379.1;
MIM; 605666; -.
             P2RY8
                       P2Y purinoceptor 8 (P2Y8).
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InterPro; IPR000276; GPCR_Rhodpsn.
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coupled receptor; Transmembrane: Glycoprotein
1 42 EXTRACELLULAR (POTENTIAL).
43 63 1 (POTENTIAL).
64 72 CYTOPLASMIC (POTENTIAL).
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29.0%; Pred. No. 8.6e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein
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PROSTTE: PS00237: G_PROTEIN_RECEP_F1_2: 1.
PROSTTE: PS50262: G_PROTEIN_RECEP_F1_2: 1.
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MEDLINE-97284734; PubMed-9139711;
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Amphibia: Batrachia; Anura, Mesobatrachia, Pipoidea; Pipidae;
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139 VHPYRGYCHPITSLRPMNAKHAYVICALVWLSVTLCLVPNLIFVTVSPKVKNTICHDTTP
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Biol. Chem. 272:12583:12590(1997).

Biol. Chem. 272:12583:12590(1997).

FURCTION: RECEPTOR FOR EXTRACELLULAR ATP, HTP, CTP, GTP AND ITP, THE ACTIVATY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLUIAR LOCATION: Integral membrane protein. SIMILARITY: BELOWS TO FAMILY LOF G-PROTEIN COMPLED RECEPTORS
                              IDRYQKTTRPEKTSNPKNLLGAKILSVVIWAEMELLSLPNMILTNRQPRDKNVKKCSELK 179
                                                                                             IIFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLIT 119
                                                                                                                               MKLLMNLTN--DTEDICVFDEGEKFLLLPVSYSAVEMVGLPLNIAAMWIFIAKMRPWNPT 78
                                                                                                                                                           MQAVDNETSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFF-QIRSKSNF 59
                                                              TVYMENLALSDTLYVLSLPTLVYYYADKNNWPFGEVLCKLVRFLFYANLYSSILFLTCIS
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N-LINKED (GLENAC. ...) (POTENTIAL)
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PF0STTE; PS00237; G_PROTEIN_RECEP_F1_1: FALSE_NEG PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAK-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                      G-protein
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                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROF entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the original conditions the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute There are no restrictions on its use, by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11591709;
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Mammalia; Eutheria; Rodentia; Schuroqnathi; Muridae; Murihae; Mus
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CYSLTK2 ek CYSLT2.
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characterization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in the spleen, thymus and adrenal gland, and lower the kidney, brain and peripheral blood leukocytes.
SIMILARITY: HELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol Chem 276-47489-47495(2001).

FUNCTION: Peopptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol calcium second messenger system. The rank order of affinities the leukotrienes is LTC4 - LTE4 - LTE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHROWLIMIAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed at low levels, with highest
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282 SCHNIFFLYYFAGENEKARI, 300
                                      291 ACLIDEFTYFFICKSFRNSL 309
                                                                                      227 KKALTT IVIAMITELLETELPYHALKTLHLVTWDKD - SCGOVLHKATVITLTMAAAN 281
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293 609 CYPTOPLASHIC (POTENTIAL).
95 171 BY SIMILARITY.
14 14 N LINKED (GLUNAC)...) (POTENTIAL).
19 AA: 45227 MW; 327B3A6EBB22A02 CKC64;
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Result
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Maximum Match 100%
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Perfect score:
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Copyright (n) 1994 - 2000 compugen Ltd
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US-09-221-456-2
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US-08-812-871-1
US-08-867-947A-29
US-08-867-947A-29
US-08-93-35-524A-2
US-08-93-35-524A-2
US-08-93-35-524A-2
US-08-86-79-47A-6
US-08-86-79-747A-6
US-08-86-79-747A-6
US-08-88-762-8-79-78-4
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TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEAABL RECEPTOR
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REGISTRATION NUMBER:
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STREET: P.O. Box 980
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US-09-558-740-2
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                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
LENGTH: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
46.3%, Score 823, DB 4, Length 333
Best Local Similarity 48.7%; Pred. No. 4.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-12-28 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/558,740 CURRENT FILING DATE: 2000-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND TITLE OF INVENTION: ANTAGONISTS OF THE HNEAA81 RECEPTOR FILE REFERENCE: GH-70318-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                     APPLICANT: Au-Young, Janice APPLICANT: Guegler, Karl APPLICANT: Muzong Cheng TITLE OF INVENTION: NOVEL HUM TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 3
                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/221,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/956,975 PRIOR FILING DATE: 1997-10-23
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CORRESPONDENCE ADDRESS:
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SZEKERES, PHILIP
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STREET: 3174 POI

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US-08-467-948A-29
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                                                        Sequence 29, Application US/08467948A Patent No. 5998164
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                    GENERAL INFORMATION:
APPLICANT: LI, YI
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INFORMATION FOR SEQ ID NO: 1:
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MOLECULE TYPE: p
IMMEDIATE SOURCE:
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: CAO, LIANG
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
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STRANDEDNESS: sin
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SOFTWARE: FastSEC
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                      LI, YI
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TINFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-MAR-1995
ATTUKNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/US95/34079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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302
                                                                                                                                                                    182 WHKASNYIEVAIPWIVELLLIVEYTAITKKIEKSHLKSSKNSTSVKKKSSKNIESIVEVE 241
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                                      306 RNSLISMLKCPNSA 319
                                                                                                           246 FICEVAPEHFAKTAYTLSÖTKOVEDCTAENTLEYVKESTUMLTSLNACUDPFTYFFI.CKSF 305
                                                                                                                                                                                                                186 WHEIVNYICOVIEWINELIVIVCYTLITKELYRSYVETEGVGKVERKKVNVKVEIIIAVE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 43.4%; Score 772; DB 2; Length 329
Local Similarity 47.5%; Pred. No. le-58;
hes 149, Conservative 60, Mismatches 105, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
IGPOLOGY: not rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                62 IVIADEVMSLTEPEKILGDSGLGPWQLNVEVCKVSAVLEYVNMYVSIVETGLISEDRYYK 121
                                                                                                                                                                                                                                                                                                                                                                                         66 TVISDLLMILTEPEKILSDAKIGTGPLRTEVCQVTSVIFYFTMYISISELGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NSTSTÖPPDESCSÖNLLITÖÖTIPVLYCMVFTAGILLNGVSGWIFFYVPSSKSFTIYLKN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 NUTSAPGNTSLCTPDYKITQVLFPLLYTVLFFVGLITNGLAMPIFFQIPSKSNFIIFLEN 65
REILCKKLHIPLKA 315
                                                                                  FVCFVPYHIARIPYTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPF
                                                                                                                                                                                                                                                           TVKPLWTSFIQSVSYSKIJ.SVIVWMIMULLAVPNIILINQSVKEVTQIKCIELKSELGRK 181
                                                                                                                                                                                                                                                                                                     TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185
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GENTZ, REINER
BULT, CAROL J.
SUTTON 111, GRANGER G.
ROSEN, CPAIG A
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                                                                                                                                                                                                                                                                                                                                                                                                    Outry Match 43.4%; Score 772; DB 3; Length 325, Hest Local Similarity 47.5%; Pred. No. 1e-58; Matches 149; Conservative 60; Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 80 MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEEFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: POSITIONS
SOFTWARE PATERIAN REPEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
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APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polyton leadlides Encoding Human G-Protein
TITLE OF INVENTION: Compled Receptor GPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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                      246 FIGEVPEHEARIPYTISOTROVEIXTAENTLEYVKESTLWLTSLNAGLDEFIYFFICKSE 305
                                                               186 WHEIVNYIGQVIEWINFLIVIVGYTLITKELYRSYVRTPGVGKVPPKKVNVKVFIIIAVF 245
                                                                                                                                               122 IVKPLWTSFIQSVSYSKILSVIVWMLMILLAVPNIILTNQSVREVTQIKGIELKSELGRK 181
                                                                                                                                                                       FILING DATE: 06:JU
                                                                                                                                                                                                                                   62 IVIADEVMSLTEPEKILGDSGLGPWQLNVEVCRVSAVLEYVNMYVSIVFEGLISEDRYYK 121
                                                                                                                                                                                                                                                                          66 TVISHLLMILTEPEKILSDAKKATAPHATEVOQVTSVIEVETMYISISELGLITIDRYQK 125
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                                                                                                                                                                                                                                                                                                                    2 NSISTOPPDESCSONILLIFOOTIPVLYCMVFTAGILLNGVSGWIFFYVPSSKSFITYLKN 61
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BULL, CAROL J
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5, ERIC K.
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30 MAR:1995
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; Patent No. 6063596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-855-0555
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123 IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 182
                                     126 TTRPFKTSNPKNLLGAKILSVVIWAFMFILLSLPNMILTNROPRDKNVKKCSFLKSEFGLV 185
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OPERATING SYSTEM:
                                                                                                                                                                                                                                  / Match 43.4%; Score 772; DH 3; Length 338;
Local Similarity 47.5%; Fred. No. 1.1e 58;
nes 149; Conservative 60; Mismatches 105; Indels
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CITY: Palo Alto
                                                                              63 IVIADEVMSLTEPEKTLGDSGLGPWQLNVEVCRVSAVLEYVNMYVSTVEEGLISEDRYYK 122
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME. Billings, Lucy J. REGISTRATION NUMBER: 36,749
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                                                                                                                                                          3 NSTSTQPPDESCSQNLLITOQ11PVLYCMVF1AG11LNGVSGW1FFYVPSSKSF11YLKN 62
                                                                                                                                                                                               6 NLTSAPGNTSECTRDYKITQVLEPLLYTVLEFVGLITNGLAMRIFFGIRSKSNFIIFLKN 65
                                                                                                     TVISDLLMILTEPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: GP50007
COURENT APPLICATION NUMBER: US/09/303,524A
COURENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,957
PRIOR FILING DATE: 1998-05-01
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APPLICANT: FOLEY, JNM

APPLICANT: FOLEY, JNM

APPLICANT: ARNOLD, ANNE ROMANIC

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND

TITLE OF INVENTION. ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001

TITLE OF INVENTION. RECEPTOR AND LIGANDS THEREOF
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TYPE: FRT
                                                                       303 REILCKKLHIPLKA 316
                                                                                                                                                                                                                                                                   183 WHKASNYIFVAIFWIVFILLIVFYTAITKKIFKSHLKSSRNSTSVKKKSSRNIFSIVFVF 242
                                                                                                                                                                                                                                                                                                                                                                      123 IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVPEVTQIKCIELKSELGPK 182
                                                                                                                                                                                                                                                                                                                                                                                                                     126 TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185
                                                                                                                                                                                                                    246 FICEVPEHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF 305
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                                                                                                                          306 RNSLISMLKCPNSA 319
                                                                                                                                                                    243 FYCFYPYHIARIPYTKSOTEAHYSCOSKEILRYMKEFTLLLSAANVCLDPLIYFFLCOPF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 RELLCKKLHIPLKA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 RNSLISMLKCPNSA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 IVIADEVMSLTEPEKILGDSGLGPWQLNVEVCRVSAVLEYVNMYVSIVEEGLISEDRYYK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 43.4%; Score 772; DH 4; Longth 338, Local Similarity 47.5%; Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 TVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVTSVIEYETMYISISELGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NSTSTOPPDESCSONLLITOOTTPVLYCMVFTAGILLNGVSGWTFFYVPSSKSFITYLKN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NUTSAPGNISLCIRDYKITQVLEPLLYIVLEFVGLIFNGLAMKIFFQIRSKSNEILFLKN 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEWART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60: Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.2%; Score 679.5; DB Best Local Similarity 43.7%; Pred. No. 9e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COMPLED REC
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                          142 KVVKPFGDSRMYSITETKVLSVCVWVIMAVLSLPNIILTNGQPTEUNIHDCSKLKSPLGV
260 VYFTCFLPYHLCKMPSTFSHLDRLLDESAQKILYYCKETTLFLSACNVCLDPTIYFFMCK 319
                                      244 VFFICEVPFHFARIPYTLSQTRDVFDCTAENTLEYVKESTLWLTSLNACLDPFIYFFLCK 403
                                                                                                                                                                                                 125 KTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGL 184
                                                                             202 KWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKS--SRQFISQSSRKRKHNQSIRVVVA 259
                                                                                                                      185 VWHETVNYTOQVTEWTNELTVTVCYTLTTKELYRSYVRTRGVGKVFEK-KVNVKVETTTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: 1650519
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TYPE: amino acid
STRANDEDNESS: sir
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REGISTRATION NUMBER: 36,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                          82 NIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYL 141
                                                                                                                                                                                                                                                                                 65 NTVISDLLMILTEPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQ 124
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                                                                                                                                                                                                                                                                                                                          25 NRSDGPGKNTTL---HNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYIK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
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Hillman, Jennifer L.
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                                                                                                                                                                                                                                                                                                        Unery Match 30.7%; Score 546.5; DB 2
Host Local Similarity 42.3%; Pred. No. 1.7e-39;
Matches 116; Conservative 45; Mismatches 104
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TELEPAX: 202-371-2540
INFORMATION FOR SEQ 1D NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING MARE: 30 MAR 1995
ALTORNEY/AGENT INFORMATION:
NAME: STEFFE ERIC K.
REGISTRATION UNMERC 46,688
REFERENCE,THOKET MIMBER, 1488
LELECOMMUNICATION UNFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
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8-467 948A 5
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TITLE OF INVENTION: Compled Receptor GPR2
NUMBER OF SEQUENCES: 30
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PRIOR APPLICATION DATA:
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    157 IFWINFLIVIVCYTLITKE
                                           135 KPVWGKTVS1F1WFFWFF1SLPNMTLSNKEATPSSVKKCASLKGPLGLKWHQMVNN1CQF 194
                                                                               187 NILICAK ILSVVIWAFMELISTENMILITNRUPROKNVKKOSELKSEEGLVWHEIVNYICOV 196
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                                                                                                                                                                                                                                          17 CTRDYKLTOVLEFILLYTVLFEVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLLMILT 76
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                                                                                                                               75 LPEKILSOSHLAPWQLKAFYCRESSVIFYETMYVGIVLLGLIAFDRELKIIRPLRNIFLK 134
                                                                                                                                                                    77 FPEKILSDAKLGTGPLKTFVCQVTSVIFYFTMYISISFLGLTTIDRYQKTTRPFKTSNPK 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
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1100 NEW YORK AVE., NW, SUITE 600
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BULL, CAROL J.
SUFTON LLL, GRANGER G.
ROSEN, CRAIG A.
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30 MAR 1995
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LYRSYVETEGVGEVERKKVNVKVFIIAVFFICFVP- 251
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                                                                                                                                                                                                                                                                               Matches 116; Conservative 45; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                     Query Match 30.7%; Score 546.5; DB 3; Length 293; Best Local Similarity 42.3%; Pred. No. 1.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540 INFORMATION FOR SEQ 1D NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/04079 FILING DATE: 30-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL I.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR1
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135 KPVWGKTVSIFIWFFWFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
                                           137 NILIGAKTISVVIWAEMELLSIPNMILITNRQPRDKNVKKCSELKSEEGIVWHETVNYTCQV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 FHILTVKPTIRLT -- - VDCKI - NCLLLKKQLSFW 284
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                                                                                                                                                                                                                                 17 CTRDYKITQVLEPILLYTVLEFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLLMILT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 1HM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                         75 LPEKTI SDSHLADWOT RAFYCHESSYTEYETMYYGTYLLGILTAFDRETKITRPLKNIFIK 134
                                                                                                                                     77 FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                   15 CPKDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFILYLKNTLVADLIMTLM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/08702344 Patent No. 5723315
                                                                                                                                                                                                                                                           Query Match 27.4%; Score 488; DB 1; Length 319; Best Local Similarity 34.5%; Pred. No. 1.8e-34; Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps
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INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BYOND, SCOTE A.
REGISTATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HAM PC COMPUTER: HAM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SECRETED PROTEINS AND FOLYNUCLEOTIDES TITLE OF INVENTION: ENCODING THEM NUMBER OF SEQUENCES: 37
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120 CKTYRTQEPGFAKMISTVVWLMVLLIMVPNMMIPIKDIKEKSNVGCMEFKKEFGRNWHLL 179
                                         130 FKTSNPKNLLGAKILSVVIWAFMELLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEI 189
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                 13 NTSLCTROYKITQVLEPLLYTVLEEVGLITNGLAMRIFFQIRSKSNFI-IFLKNTVISOL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                      62 LITLALPVKIVVD--1.GVAPWKLKIFHCQVTACLIYINMYLSIIFLAFVSIDRCLQLTHS 119
                                                                                                                                72 LMILITEPEKILSDAKLGTGP--LRTEVCQVTSVIFYFTMYISISELGLITIDRYQKTTRP 129
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                                                                                                                                                                          3 NSSFECPVYKULEP-ETYPEYLVELVGIIGSCEATWAETQKNTNHRCVSIYLINLLTADE 61
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Treacy, Maurice
Spaulding, Vikki
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; Patent No. 5508384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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NAME: TOWNSEND, KEVIN G.
REGISTRATION NUMBER: 34,033
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                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER MITTELECOMMUNICATION INFORMATION: 202-628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHAPACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 VNYLCQVIFWINF-LIVIVCYTLITKELYRSYVRTRGVGKVPR-KKVNVKVFILLAVFFI 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 CFYPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRN 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLEFAX: Lui
TELEFAX: 248633
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                      145 SVVIW-----AFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFG----LVWHEIVNYIC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 09-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                               61 SNQGNWFLFKFLCNLAGCLFFINTYCSVAFLGVITYNFFQAVKYFIKTAQATTRKRGIAL 120
                                                                                                       85 AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                       27 LEPLLYTVLFEVGLITNGLAMRIFFQI-PSKSNFI-IFLKNTVISDLLMILTFPFK1LSD 84
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                 1 LEPIVYSIIEVIGIIANGYVLWVEARLYPSKKNEIKIEMVNLTVADLLELITLPLWIVYY 60
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single
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                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            MOTEUM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/OWNKET NUMBER: 44,044
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                         145 SVVIW
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COMPUTER: IBM PC computible
OPERATING SYSTEM: PC DOS/MS DOS
                                                                61 SNOGNWELPKELCINLAGCLEEINTYCSVAFLGVITYNREQAVKYPIKTAQATTRKRGIAL 120
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                                                                                                           85 AKEGIGIPLKTEVOOVTSVIEVETMYLSISELGILITIDKYQKTTKPEKTSNEKNILIGAKII, 144
                                                                                                                                                                                              27 LEPILYTVIFEVGLIINGLAMKIEFQI-KSKSNEI IFLKNIVISDLLMILTEPEKILSD 84
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32.2%; Pred. No. 7.7e-28;
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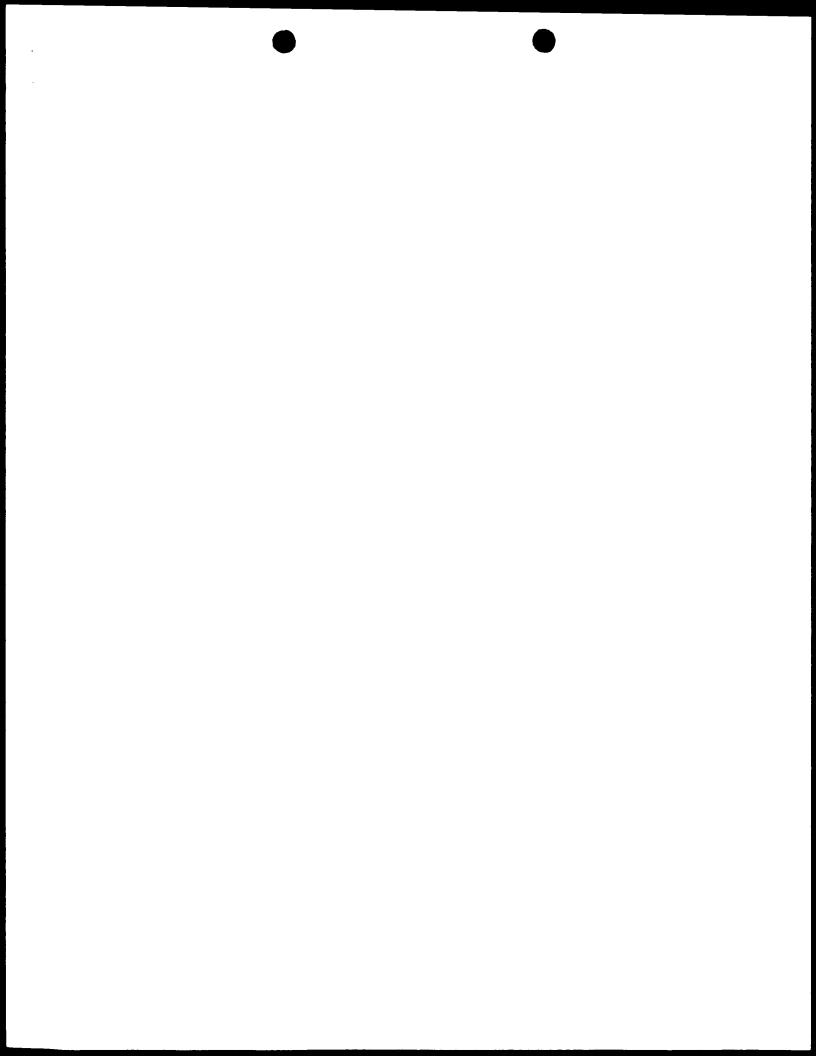
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/08988876
Matches 103; Conservative
                       Best Local Similarity
                                     Query Match
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                                                                                                                                                                                                                                                                                                                                              TELEPHONE. 650 855-0555
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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CITY: Palo Alto
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TITLE OF INVENTION: WITH IMMUNE RESPONSE
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APPLICANT: Bandman, Ol
                                                                                                                                                           IMMEDIATE SOURCE:
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                                                                                                                     LIBRARY: Gen
CLONE: 49443
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                     22.1%; Score 392.5; DB 3; Length 342; 30.7%; Pred. No. 2.8e-26;
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                                                          243 ICEVPHHMVQLPWTLAEL-GMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFR 301
                                                                                                                            189 -----ICIVLGFFIVFILILFCNI.VIIHTILLRQPVKQQRNAEV-RRRALMMVCTVLAVFV 242
                              307 NSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                                                                                                    188 EIVNYICQVI-FWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFF 246
                                                                                                                                                                                                                                                             70 LPLWIVYYSNOGNWELPKELCNLAGGLEFINTYCSVAFLGVITYNREQAVKYPIKTAQAT 129
                                                                                                                                                                                                                                                                                 77 FPPKILSDAKIGTGPLRTFYCQVTSVIFYFTMYISISFLGLITTDRYCKTTRPFKTSNPK 136
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Search completed: August 21, 2002, 15:45:23 Job time: 191 sec



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GenCore version 4.5

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Database
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2. /SIDSI/gcgdata/hold-genesedy-genesedp-embl/AA1991 hAT *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		<b>%</b> ©uery				
<b>X</b> O.	Score	Match	Match Length DB	DB	ID	Description
_	1778	100.0	342	20	AAW81576	ia-5 pesupui-ARR
2	1778	100.0	34.2	۲,	AAY71306	Human orphan G pro
w	1778	100.0	342	۲,	AAB02840	Human G protein
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5	1778	100.0	3 <b>4</b> 2	t) t)	AAM79249	Human protein SE
σ.	1778	100 0	342	13	AAE04386	Human P2 burinera
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œ	1634	91.9	315	t)	AAE04385	Human P2 buriner
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10	1493.5	84.0	387	21	AAY94498	Rat MP-10 recept
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## ACIGNMENTS

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AAW81576
                                                                                                                                                       RESULT
                                                                                                                  AAW81576 standard, Protein; 342 AA.
EBV-induced G-protein coupled receptor (EBI-2) polypeptide.
                                       22.FEB-1999 (first entry)
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EBV-induced G-protein coupled receptor; EBI-2: Epstein-Barr Virus; ulcer; endothelium-differentiation gene. EDG-1-like G-protein coupled receptor; recombinant; agonist; asthma, Farkinson's disease, heart failure, asthma, hypotension; urinary retention; osteoporosis; antagonist; hyportension; angina pectoris; myocardial infarction; allergy, psychosis; depression; migraine; vomiting; stroke; eating disorder; migraine headache; cancer; prostatic hypertrophy; detection; drug screening.

Homo sapiens

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07-MAY-1997;
           U7-MAY-1998;
                                         Misc-difference 14
                    12-NUV-1998.
                             WO9850549-A2
                                                  Misc-difference
  9705-0852824
           98MO-US03048
                                                      Location/Qualifiers
                                     /note= "encoded by AAC"
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Human orphan G protein coupled receptor hCHN8
                                                                         02 NOV 2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to transform host cells for the recombinant production of the proteins. Advantsts for G-protein coupled receptors can be used for the treatment of asthma, Parkinson's disease, acute heart failure, hypotension, urinary retention and osteroporosis. Antagonists can be used for the treatment of hyperfension, angina pectoris, myocardial infarction, ulcers, asthma, allerdies, psychoses, depression, migraine, vomiting, stroke, eating districtions are considered as the constitution of the 
                                                                                                                                                                                                                                                      AAY71306 standard; Protein; 342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1: Fig 1A C; 65pp; English.
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products for treating e.g. asthma, Parkinson's disease, heart
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1 MOAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFYGLITNGLAMRIFFQIRSKSNFI 60

Best Local Similarity
Matches 342; Conser

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29-SEP-1999;
01-07T-1999;
U1-07T-1999;
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116-FFB-1999
26-FFB-1999
112-MAR-1999
112-MAR-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
                                                                                                                                                                                   alpha helices with an extracellular N terminus and an intracellular c-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCKs may be used in the identification of their endogenous ligands, and to screen potential GPCE adjoints and antavousists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCKs may be used tor tissue localisation expression analysis to provide information about their function in healthy and pathological states.
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      length EST (expressed sequence tag) 764455 as a probe.
The orphan GPCP of the invention, like all GPCPs has seven transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        orphan G protein coupled receptor (GPCP), expressed in left and right cerebellum, kidney and lung. The hCHN8 cDNA was identified using full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present amino acid sequence is the hCHN8, an endogenous human orphan G protein coupled receptor (GDCP), expressed in left and right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 62; Page 82-83; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human orphan 6 protein compled teceptors and the encoding conas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1999;
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29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for use in the identification of G protein-coupled receptor agonists
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100.0%; Score 1778; DH 21; Length 342; Larity 100.0%; Pred No. 4.2e-1B7; Conservative 0; Mismatches 0; Indels 0;
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                                                          Key
                                                                                                                                                       Human; G-protein-coupled receptor; GPCP: 15625 receptor protein; glial cells; spleen; colon; liver; brain; T-cell; heart; red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
                                                                                                                                                                                                                                       Human 15625 receptor protein
                                                                                                                                                                                                                                                                                                                                                             AAY94444 standard, protein; 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02865 to AAB02869 represent sequences used the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCK receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes transmembrane receptors, preferably
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                                                                                                  Homo sapiens
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                                                                                                                                      thrombocytopenia, gene therapy; ss
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Best Local Similarity
                                                                                                                                                                                           The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.
                                                                                                                                                                                                                                                                              The present sequence shows the 15625 receptor protein, It is a novel of coupled profein receptor (GPCR). The CDNA for this protein was isolared by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein.
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                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL.) MILLENNIUM PHARM INC
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                                       1 MOAVONLTSAPONTSLOTROYKITQVLFPILLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                           d receptor useful for screening a cell derived from a subject disorders such as anaemia, neutropenia and thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998;
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13
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                                                                                                            100.0%; Score 1778; DB 21; 100.0%; Pred. No. 4.2e-187;
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                                                                                                                            DB 21; Length 342;
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activity, tissue growth factor activity, immunomodulatory

activity and

production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating

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20-JUN-2000;
19-JUL-2000;
                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elatic cytokine, cell proliteration or cell differentiation or which may income
                                                                                                                                                                                                                Tang YT,
Zhao QA,
                                                                                                     Claim 20; Page 4310, 6221pp; English.
                                                                                                                               useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein SEQ ID NO 1911.
                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                                                                                                 N-PSDB; AAK52382
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20-OCT-2000;
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                                                                                                                                                                                                     Yang Y, Wejhrman T,
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2000US-0620325.
2000US-0654936.
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2000US-0693325
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lang J, Ren F,
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Best Local :
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                  Domain
                                                    Doma i n
                                                                                                                                                                                                                                                                                   Gi; disseminated intravascular coagulation; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human P2-purinergic receptor subtype, P2Y12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2001 (first entry)
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                                                                                                                         Doma i n
                                                                                                                                                             Doma i n
                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE04386 standard: Protein:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: keeperds for SFg 10 NG 2310 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are unitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                    thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation.
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                                                                                /label-
140...162
             /label= Transmembrane_domain_5
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97...121
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27..50
/label = Transmembrane_domain_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, precelampsia, deep venous thrombosis, embulism, dissentifated intravasculat coagulation, thrombotic thrombosis, embulism, dissentifated intravasculat coagulation, thrombotic restenotic complications following angioplasty, carotid endarterectomy, post CABG (coronary artery bypass grait) surgery, vascular grait surgery, stent placements or insertion of endovascular devices and prostheses. P2Y12 receptor is useful for identifying binding partners and for dagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelei aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is human P2-purineratic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purincryic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin sensitive G protein (Gi). P2Y12 receptor is a G protein coupled receptor that responds to ADP. The invention also relates to a method for that responds to ADP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
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342; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to ADP (adenosine 5' diphosphate) receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human P2-purinergic as P2Y12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The 1952's receptor protein is a novel 6-coupled protein receptor (GPCR). The CNNA for this protein was isolated by screening a human CNNA library with sequences homologous to other GPCRs. The 19625 receptor protein is expressed in the glial cells of the brain. It is also expressed in serveral other tissues, the 1962's receptor protein may be useful for producing antibodies which can be used to detect the presence of the
                                                                                                                                                                                                                                                                                                                                                into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia. The
                                                                                                                                                                                                                                                                                                                                                                                                      receptor protein. The 15625 receptor protein polynucleotides are useful for generaling probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 3 protein coupled receptor; GPCR; 15625 receptor protein; 41ial cells; spleen; colon; liver; brain; T cell; heart; red cell; thymus; B cell; pancreas; disorder; chromosome 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure: Page 90 92; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dentitying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N PSDB; AAA27127
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                                                                                                                                                                                                                                                                                                                                   DI 658-01
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                                                                                                                                                                                    Local Similarity
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7#5 '85
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                                                                                                                                                                                                                                                          Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful tor identitying binding partners and for diagnostic applications
                                                                                                                                                                                                                                                                                                                N-PSDB; AADU8694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE04385 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                            (CORT-) COR THERAPEUTICS INC.
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                                                                                                                                                                                                                                                                                                                                                                             Ramakrishnan-Dubridge V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiant, vasotropic; thrombolytic
                                                                                                                                                                                                                                                                                                                                                                             Julius DJ;
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thromborytopaenic purpura or a bleeding disorder; thrombotic and restenotic complications following angiopiasty, carotid endarterectomy

(coronary artery bypass graft)

sufferly, Vasculat

graft surgery,

infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, preeclampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial

selectively in the platelets and brain, and couples to a pertussis toxin-sensitive G protein (GI). FIYIZ receptor is a G protein coupled receptor as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor i the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed

The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed

Example 1; Page 84-85;

108pp; English.

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                                                                                                                                                                                                                                                                                                                                                    Rat; P2-purinergic receptor, P2Y12, cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; AlD; adenosine 5' diphosphate; angina; myocardial infarction ischammic attack, proeclampsia, bleeding lisurder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; vascular injury; schizophrenia; eating disorder; depression; angioplasty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is a fragment of human P2-purineraic receptor subtype, referred as P2Y12.
Conley PB,
                                                                                                                                                                                                                                                                                        peripheral vascular disease; platelet aggregation, restanctic, embolism thrombocytoperate parpara, strake; pertussis texin sensitive G protein; Gi; disseminated intravascular coagulation; thrombosis.
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                                        (CORT-) COR THERAPEUTICS INC
                                                                                    23-DEC-1999;
                                                                                                                            26-DEC-2000; 2000WO-US34998.
                                                                                                                                                                       28-JUN-2001
                                                                                                                                                                                                               WO200146454-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCKSFRNSLISMLKC 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 AA;
Jantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                  9908-0171622
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Ramakrishnan-Dubridge V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1634, DB 22,
k; Pred No. 2.6e-171;
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Julius DJ;
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                                                                                                                                                                                                                                                                                                                                       embolism;
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AAY94498

AAY94498 standard; protein; 387 AA

Rat MP-10 receptor protein

15-SEP 2000 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rne invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2'-purinergic receptor. The F2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin sensitive G protein (G1). P2Y12 receptor is a G protein coupled receptor that responds to ADP. The invention also relates to a method for identifying a perturbation and coupled as to ADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is rat P2-purinergic receptor subtype, referred as P2Y12 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombocytopaenic purpura or a bleeding disorder, thrombotic and restenotic complications following anglopiasty, calotid endarterectomy, post CABG (coronary artery bypass graft) surgery, vascular graft surgery, stent placements or insertion of endovascular devices and prostheses. P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, precelampsia, deep venous thrombosis, embolism, disseminated intravascular coaquiation, thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 81-82; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AADUB693.
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     312
                                                                                                                                                                                                        306 RNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                                                  {\tt 252\ ficfvpfhfaripytlsqtravfdcnaentlfyvkestlwltslnaeldpfiyfflcksf}
                                                                                                                                                        246 FICEVPEHFARIPYTLSOTROVFDCTAENTLEYVKESTLWLTSLNACLDPFIYFFLCKSF
                                                                                                                                                                                                                                                                 186 WHETVNYTCOVIFWINFLIVIVCYTETTKELYRSYVRTRGVGKVPRKKVNVKVFTITAVF
                                                                                                                                                                                                                                                                                                                                                                         126 TIRPEKTSNPKNULGAKILSVVIWAFMFLLSLENMILTNRGFRUKNVKROSFLKSEFGLV 185
                                                                                                                                                                                                                                                                                                                                                                                                                            72 tvisdllmiltfpfkilsdaklgaghlrtlvcqvtsvtfyftmyisisflglitidrylk 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 TVISDLIMTLTEPEKILSDAKLGTGPLRTEVCQVTSVIFYETMYISISELGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 nttsipgtstlcsrdykitqvlfpllytvlffaglitnslamriffqirsksnfiiflkn 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 NITSAPGNTSICTRDYKITQVLEPLLYTVI.FFVGI.ITNGLAMRIFFVGIRSKSNFIIFIKN 65
rnslmsmlrc----stsgankkkggeggdpseetpm 343
                                                                                                                                                                                                                                                                                                                       ttrpfktsspsullgakilsvaiwafmfllslpnmiltnrrpkdkditkcsflksefglv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.9%; Score 1528.5; 86.9%; Pred. No. 1.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to ADP (adenosine 5'-diphosphate)
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AAE04 (B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor protein is useful for identitying new anaesthetic and analgesic agents. Such agents may be identified using assays designed to detect agentists capable of binding to the receptor, therefore modulating intracellular signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N PSDH: AAA48642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification of new anaesthetic and analgesic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Almad S. Hoffert C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is rat MP-10 receptor protein. The DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASTR ) ASTRA PH
(ASTR ) ASTRA AH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 tvisdlimilttptkilsdaklgaghlrtlvcqvtsvtfyftmyisisflglitidrylk 131
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                                                                                                                                                                                                                                                                tictopthtarapytlsqtravtdenaentlfyvkestlwitsInaeldpfiyffleksf
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Query Match 69.6%; Best Local Similarity 95.7%;

Score 1237.5; DB 2: Pred. No. 9.4e-128; Mismatches

DB 22; Length 267; Indels

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Conservative

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identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, precelampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic thrombotytopacnic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, post CARG (coronary artery bypass grait) surgery, vascular grait surgery, stent placements or insertion of endovascular devices and prostheses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding (DNA molecule, P2Y12 receptor is the subtype of P2-purincergic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for
                                                                                                                                                                                            P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring
Sequence
                                                         receptor subtype, P2Y12 truncated allelic variant. The variant is obtained by deleting two bases 'CA' from position 789-790 of the wildtype numan P2Y12 receptor cDNA, resulting in amino acid changes from position
                                                                                                                             compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is human P2-purinergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 29; Page 91 92; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications {\bf r}_{\rm c}
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                                           240 of the wildtype human P2Y12 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORT-) COR THERAPEUTICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopachic purpura; stroke; pertussis toxin-sensitive G protein; G1; disseminated intravascular coagulation; thrombosis; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2000; 2000WO-US34998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human P2 purinergic receptor subtype, P2Y12 truncated allelic variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE04387 standard; Protein; 267
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neurological disease: Alzheimer's disease: trauma; wounding; spinal cord injury; skeletal disorder; cytostatic; immunosuppressive; anti-HIV; anti-Inflammatory; anti-Arthritic; anti-Interiosclerotic; neuroprotective; vulnorary; antiallergic; antimicrobial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECX protein; human; secreted; membrane-associated; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human chemokine receptor-like protein, SECX 2777610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation regulator; differentiation regulator; non-malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune disorder; autoimmune disease; transplant rejection; allergy: AIDS; intection; inflammatory disorder; arthritis; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                      Novel human membrane associated or secreted polypeptides and polynucleotides useful for diagnosis, prevention and treatment of pathological states such as cancer, immune, cardiovascular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2000; 2000Wo-US05280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological; gene therapy.
                               proteins of the invention are either secreted or membrane-associated proteins and act as regulator of cellular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnosing
                                                                                                                                                                                                                     Claim 1; Fig 1; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA93616
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                                                                                                                                                                                                                                                                                              neurological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IFLKNTVISDLLMILTEPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI 120
                                                                                                                                               Sequences AAB23029-B23048 represent human SECX proteins. The SECX
   the presence of, or predisposition to, a disease associated with altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulate SECX expression (e.g., using antisense oligonucleotides). SECX nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides and for screening tissue cultures for contamination. Diseases that may be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used detect SECX mRNA or genetic lesions in the SECX gene. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   levels of SECX proteins and nucleotides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autonomous diseases, transplant rejection, allorgies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skin disorders, cardiovascular disorders, atheroselerosis, restemosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                 Human; G protein coupling receptor; CNS; central nervous system.
                                                                                                                                                                                                                                             Human G protein coupling receptor
                                                                                                                                                                                                                                                                                                                                     AAB74397;
                                                                                                                                                                                                                                                                                                                                                                                AAB74397 standard; Protein; 333 AA
                     17-AUG-1999,
                                                                                                              JP2001054389-A
                                                                                                                                                                                                                                                                                            11-JUL-2001 (first entry)
                                                                   27-FEB-2001.
                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 rkttassqenbssqtd 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 lpfkilsdshlapwqlrafverfssvifyetmyvgivligliafdrflkiirplrniflk 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 FPFKILSDAKLGTGPLRTFVCQVTSV*FYFTMY1SISFLGL1TIDRYQKTTRPFKTSNPK 136
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                       99JF-0230777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57, Mismatches 102;
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                                                                       06 FEB 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lamily and a method for screening using the receptor. The invention be used for screening of agents expected to be useful for prevention and treatment of central nervous system (CNS) diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a novel C protein coupling receptor, a demonstrating for the receptor family, a process for preparation of the receptor family, an antibody to the receptor
24 JUI 1999;
                                 23 JUL 1999;
                                                                                                           JP2001029083 A.
                                                                                                                                              Homo sapieus
                                                                                                                                                                                  schizophrenia, Parkinson's disease
                                                                                                                                                                                                                                        Novel human G protein coupled receptor.
                                                                                                                                                                                                                                                                                                                       AAB74494;
                                                                                                                                                                                                                                                                                                                                                       AAB74494 Standard; Protein; 333 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present sequence the C protein coupling receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 rkttassgenhssqtd 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 CIRDYKITOVLEFULLYTVLEFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLLMILT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 FIFKILSDAKLGIGDLRIFYOGVISVIFYFIMYISISFIGLIIIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kpvtaktvsitiwttltfislpnmilsnkeatpssvkkeaslkgplglkwhgmvnnicqf 194
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                               8166070 df66
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49.1%; Pred. No. 1.1e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.6%; Score 829; DH 22; Best Local Similarity 49.1%; Pred. No. 1.1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
  Domain
                                                              Domain
                                                                                                                                                                                                                    attention deficit hyperactivity disorder, neurasthemia; semile dementia; affective disorder, neuropathy, Alzheimer's disease; Farkinson's disease;
                                                                                                                                                                                                                                                              Human; G protein coupled receptor; GPCk; CONZO3 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychiatric disease; neurosis; anxiety; neuritis;
                                                                                                                                                                                                                                                                                                                                              Human CON203 G protein coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel human G protein coupled receptor. This is useful in the identification of treatments for central nervous system diseases such as schizophrenia, Parkinson's disease and aches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 11; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new G protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                    Domain
                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                       depression; migraine; genetic screening;
                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE02494 standard; Protein; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF81501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISMLKCP 316
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                                                                                                Location/Qualifiers
29..53
/label- Intracellular_domain
/note: "First IC loop"
63..82
                                                         /label- Transmembrane_domain_(1TM)
54..62
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99US-0429517.
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/note= "First EC loop"
97..118
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/note= "Third EC loop"
281..300
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"Phird IC loop"
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Seven transmembrane receptor polypeptides and polynucleotides, useful tor treating neurological or psychiatric disorders, e.g. schizophrenia, for identifying compounds useful for treating schizophrenia

Claim 1; Page 10-11; 215pp; English

is also useful for identifying compounds useful for treating schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder/ attention deficit disorder, epilepsy, neuritis, neurasthenia, neuropathy, neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present sequence is human CON203 G protein coupled receptor (GPCR) protein. The invention relates to human G protein-coupled receptor (GPCR) and their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein-coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein

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Best Local
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313 rkttassgenhssgtd 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                               kpvfaktvsifiwvflvfislpnmilsnkeatpssvkkeaslkgplylkwhqmvnnieqf 194
                                                                                                                                                                                                                                          NILGAKTISVVTWAFMFLLSLPNMTLTNRQPRDKNVKKCSFLKSEFGLVWHETVNYTCQV 196
                                                                                                                                                                                                                                                                        lpfkilsdshlapwglrafverfssvifyetmyvgivllgliafdrflkiirplrniflk 134
                                  NSATSLSQDNRKKEQD 332
                                                                                                                                     ifwtgfilmlvfyvviakkvydsyrkskskdrknnkklegkvfvvvavffvctapfhlar
                                                                                                                                                                       IFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICEVPFHFAR 256
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            46.5%; Score 827; DB 22; 48.7%; Pred. No. 1.9e-82;
                                                                                                                                                                                                                                                                                                                                                                                                             57; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 333;
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Search completed: August 21, 2002, 15:45:62 Job time: 385 sec

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